Considered on


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=> fil capl; d que l3
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FILE COVERS 1907 - 9 Dec 2002  VOL 137 ISS 24
FILE LAST UPDATED: 8 Dec 2002  (20021208/ED)

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the CAS Roles thesaurus (/RL field) in this file.


L1            41 SEA FILE=CAPLUS ABB=ON  KASSNER P?/AU
L2            17 SEA FILE=CAPLUS ABB=ON  AULT RICHE D?/AU
L3             1 SEA FILE=CAPLUS ABB=ON  L1 AND L2


=> fil wpids; d que l28
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MOST RECENT DERWENT UPDATE:     200278        <200278/DW>
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L26           18 SEA FILE=WPIDS ABB=ON  KASSNER P?/AU
L27            6 SEA FILE=WPIDS ABB=ON  AULT RICHE D?/AU
L28            1 SEA FILE=WPIDS ABB=ON  L26 AND L27


=> fil jic; d que 148; d que 149
FILE 'JICST-EPLUS' ENTERED AT 11:41:37 ON 09 DEC 2002
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FILE COVERS 1985 TO 2 DEC 2002 (20021202/ED)

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L48             0 SEA FILE=JICST-EPLUS ABB=ON  KASSNER P?/AU


L49             0 SEA FILE=JICST-EPLUS ABB=ON  AULT RICH?/AU
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=> fil biosis; d que l68; d que l78
FILE 'BIOSIS' ENTERED AT 11:41:39 ON 09 DEC 2002
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FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 4 December 2002 (20021204/ED)

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L66            22 SEA FILE=BIOSIS ABB=ON  KASSNER P?/AU
L67            18 SEA FILE=BIOSIS ABB=ON  AULT RICHE D?/AU
L68             0 SEA FILE=BIOSIS ABB=ON  L66 AND L67
```

```
L66            22 SEA FILE=BIOSIS ABB=ON  KASSNER P?/AU
L67            18 SEA FILE=BIOSIS ABB=ON  AULT RICHE D?/AU
L70         44419 SEA FILE=BIOSIS ABB=ON  LIBRAR?
L71         47285 SEA FILE=BIOSIS ABB=ON  NEST###
L78             1 SEA FILE=BIOSIS ABB=ON  (L66 OR L67) AND (L70 OR L71)
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=> fil medl; d que 191; d que 193
FILE 'MEDLINE' ENTERED AT 11:41:40 ON 09 DEC 2002
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FILE LAST UPDATED: 23 NOV 2002 (20021123/UP). FILE COVERS 1958 TO DATE.

On June 9, 2002, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/summ2003.html for a description on changes.

If you received SDI results from MEDLINE on October 8, 2002, these may have included old POPLINE data and in some cases duplicate abstracts. For further information on this situation, please visit NLM at: http://www.nlm.nih.gov/pubs/techbull/so02/so02_popline.html

To correct this problem, CAS will remove the POPLINE records from the MEDLINE file and process the SDI run dated October 8, 2002 again.

Customers who received SDI results via email or hard copy prints on October 8, 2002 will not be charged for this SDI run. If you received your update online and displayed answers, you may request a credit by contacting the CAS Help Desk at 1-800-848-6533 in North America or

614-447-3698 worldwide, or via email to help@cas.org

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L89          17 SEA FILE=MEDLINE ABB=ON  KASSNER P?/AU
L90           7 SEA FILE=MEDLINE ABB=ON  AULT RICHE D?/AU
L91           0 SEA FILE=MEDLINE ABB=ON  L89 AND L90



L89          17 SEA FILE=MEDLINE ABB=ON  KASSNER P?/AU
L90           7 SEA FILE=MEDLINE ABB=ON  AULT RICHE D?/AU
L92        3435 SEA FILE=MEDLINE ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L93           1 SEA FILE=MEDLINE ABB=ON  (L89 OR L90) AND L92


=> fil biotechno; d que l114; d que l116
FILE 'BIOTECHNO' ENTERED AT 11:41:42 ON 09 DEC 2002
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FILE LAST UPDATED: 3 DEC 2002       <20021203/UP>
FILE COVERS 1980 TO DATE.

>>>  SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN
     /CT AND BASIC INDEX  <<<


L113          9 SEA FILE=BIOTECHNO ABB=ON  KASSNER P?/AU
L114          2 SEA FILE=BIOTECHNO ABB=ON  L113 AND DETECTION/TI



L113          9 SEA FILE=BIOTECHNO ABB=ON  KASSNER P?/AU
L115          4 SEA FILE=BIOTECHNO ABB=ON  AULT RICHE D?/AU
L116          0 SEA FILE=BIOTECHNO ABB=ON  L113 AND L115


=> dup rem l93,l78,l114,l3,l28
FILE 'MEDLINE' ENTERED AT 11:41:44 ON 09 DEC 2002

FILE 'BIOSIS' ENTERED AT 11:41:44 ON 09 DEC 2002
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PROCESSING COMPLETED FOR L93
PROCESSING COMPLETED FOR L78
PROCESSING COMPLETED FOR L114
PROCESSING COMPLETED FOR L3
PROCESSING COMPLETED FOR L28
L137          5 DUP REM L93 L78 L114 L3 L28 (1 DUPLICATE REMOVED)
                ANSWER '1' FROM FILE MEDLINE
                ANSWER '2' FROM FILE BIOSIS
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ANSWERS '3-4' FROM FILE BIOTECHNO
ANSWER '5' FROM FILE CAPLUS

=> d ibib ab 1-5

L137 ANSWER 1 OF 5 MEDLINE
ACCESSION NUMBER: 2000331249 MEDLINE
DOCUMENT NUMBER: 20331249 PubMed ID: 10872445
TITLE: Inorganic polyphosphate: a molecule of many functions.
AUTHOR: Kornberg A; Rao N N; **Ault-Riche D**
CORPORATE SOURCE: Department of Biochemistry, Stanford University School of Medicine, California 94305-5307, USA..
akornber@cmgm.stanford.edu
SOURCE: ANNUAL REVIEW OF BIOCHEMISTRY, (1999) 68 89-125. Ref: 109
Journal code: 2985150R. ISSN: 0066-4154.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000712

AB Inorganic polyphosphate (poly P) is a chain of tens or many hundreds of phosphate (Pi) residues linked by high-energy phosphoanhydride bonds. Despite inorganic polyphosphate's ubiquity--found in every cell in nature and likely conserved from prebiotic times--this polymer has been given scant attention. Among the reasons for this neglect of poly P have been the lack of sensitive, definitive, and facile analytical methods to assess its concentration in biological sources and the consequent lack of demonstrably important physiological functions. This review focuses on recent advances made possible by the introduction of novel, enzymatically based assays. The isolation and ready availability of Escherichia coli polyphosphate kinase (PPK) that can convert poly P and ADP to ATP and of a yeast exopolyphosphatase that can hydrolyze poly P to Pi, provide highly specific, sensitive, and facile assays adaptable to a **high-throughput** format. Beyond the reagents afforded by the use of these enzymes, their genes, when identified, mutated, and overexpressed, have offered insights into the physiological functions of poly P. Most notably, studies in E. coli reveal large accumulations of poly P in cellular responses to deficiencies in an amino acid, Pi, or nitrogen or to the stresses of a nutrient downshift or high salt. The ppk mutant, lacking PPK and thus severely deficient in poly P, also fails to express RpoS (a sigma factor for RNA polymerase), the regulatory protein that governs > or = 50 genes responsible for stationary-phase adaptations to resist starvation, heat and oxidant stresses, UV irradiation, etc. Most dramatically, ppk mutants die after only a few days in stationary phase. The high degree of homology of the PPK sequence in many bacteria, including some of the major pathogenic species (e.g. Mycobacterium tuberculosis, Neisseria meningitidis, Helicobacter pylori, Vibrio cholerae, Salmonella typhimurium, Shigella flexneri, Pseudomonas aeruginosa, Bordetella pertussis, and Yersinia pestis), has prompted the knockout of their ppk gene to determine the dependence of virulence on poly P and the potential of PPK as a target for antimicrobial drugs. In yeast and mammalian cells, exo- and endopolyphosphatases have been identified and isolated, but little is known about the synthesis of poly P or its physiologic functions. Whether microbe or human, all species depend on adaptations in the stationary phase, which is truly a dynamic phase of life. Most research is focused on the early and reproductive phases of organisms, which are rather brief intervals of rapid growth. More attention needs to be given to the extensive period of maturity. Survival

of microbial species depends on being able to manage in the stationary phase. In view of the universality and complexity of basic biochemical mechanisms, it would be surprising if some of the variety of poly P functions observed in microorganisms did not apply to aspects of human growth and development, to aging, and to the aberrations of disease. Of theoretical interest regarding poly P is its antiquity in prebiotic evolution, which along with its high energy and phosphate content, make it a plausible precursor to RNA, DNA, and proteins. Practical interest in poly P includes many industrial applications, among which is the microbial removal of Pi in aquatic environments.

L137 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:27263 BIOSIS
DOCUMENT NUMBER: PREV200000027263
TITLE: Genetic selection of phage engineered for receptor-mediated gene transfer to mammalian cells.
AUTHOR(S): **Kassner, Paul D. (1)**; Burg, Michael A. (1); Baird, Andrew (1); Larocca, David (1)
CORPORATE SOURCE: (1) Selective Genetics, Inc., 11035 Roselle Street, San Diego, CA, 92121 USA
SOURCE: Biochemical and Biophysical Research Communications, (Nov. 2, 1999) Vol. 264, No. 3, pp. 921-928. ISSN: 0006-291X.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Although phage display is a powerful way of selecting ligands against purified target proteins, it is less effective for selecting functional ligands for complex targets like living cells. Accordingly, phage display has had limited utility in the development of targeting agents for gene therapy vectors. By adapting a filamentous bacteriophage for gene delivery to mammalian cells, however, we show here that it is possible to screen phage **libraries** for functional ligands capable of delivering DNA to cells. For example, when targeted with epidermal growth factor (EGF), M13 bacteriophage were capable of delivering a green fluorescent protein (GFP) gene to EGF receptor bearing cells in a ligand-, time-, and phage concentration-dependent manner. The EGF-targeted phage transduced COS-1 cells in a highly specific manner as demonstrated by competition with excess free EGF or alternatively with anti-EGF receptor antibodies. We further demonstrate that EGF-phage can be selected, by their abilityto transduce EGF receptor bearing cells from **libraries** of peptide display phage. When phage were incubated with COS-1 cells, EGF ligand-encoding sequences were recovered by PCR from FACsorted, GFP-positive cells and the EGF-displaying phage were enriched 1 million-fold by four rounds of selection. These data suggest the feasibility of applying molecular evolution to phage gene delivery to select novel cell-specific DNA-targeting ligands. The same approach could be used to select genetically altered phage that are specifically designed and evolved as gene therapy vectors.

L137 ANSWER 3 OF 5 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 2000:30777806 BIOTECHNO
TITLE: **Detection** of antibody display phage without clearing of bacterial culture
AUTHOR: Phipps M.L.; Xu X.; Nock S.; **Kassner P.D.**
CORPORATE SOURCE: Dr. P.D. Kassner, Zyomyx Inc., 3911 Trust Way, Hayward, CA 94545, United States. E-mail: pkassner@zyomyx.com
SOURCE: BioTechniques, (2000), 29/4 (737-740), 6 reference(s) CODEN: BTNQDO ISSN: 0736-6205
DOCUMENT TYPE: Journal; (Short Survey)
COUNTRY: United States
LANGUAGE: English

Searched by Barb O'Bryen, STIC 308-4291

L137 ANSWER 4 OF 5 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 1997:27329885 BIOTECHNO
TITLE: **Detection** of functional nicotinic receptors blocked by .alpha.-bungarotoxin on PC12 cells and dependence of their expression on post-translational events
AUTHOR: Blumenthal E.M.; Conroy W.G.; Romano S.J.; **Kassner P.D.**; Berg D.K.
CORPORATE SOURCE: D.K. Berg, Department of Biology, University of California, 9500 Gilman Drive, San Diego, CA 92093, United States.
SOURCE: Journal of Neuroscience, (1997), 17/16 (6094-6104), 62 reference(s)
CODEN: JNRSDS ISSN: 0270-6474
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A major class of nicotinic receptors in the nervous system is one that binds .alpha.-bungarotoxin and contains the .alpha.7 gene product. PC12 cells, frequently used to study nicotinic receptors, express the .alpha.7 gene and have binding sites for the toxin, but previous attempts to elicit currents from the putative receptors have failed. Using whole-cell patch-clamp recording techniques and rapid application of agonist, we find a rapidly desensitizing acetylcholine-induced current in the cells that can be blocked by .alpha.- bungarotoxin. The current amplitude varies dramatically among three populations of PC12 cells but correlates well with the number of toxin- binding receptors. In contrast, the current shows no correlation with .alpha.7 transcript; cells with high levels of .alpha.7 mRNA can be negative for toxin binding and yet have other functional nicotinic receptors. Northern blot analysis and reverse transcription-PCR reveal no defects in .alpha.7 RNA from the negative cells, and immunoblot analysis demonstrates that they contain full-length .alpha.7 protein, although at reduced levels. Affinity purification of toxin-binding receptors from cells expressing them confirms that the receptors contain .alpha.7 protein. Transfection experiments demonstrate that PC12 cells lacking native toxin-binding receptors are deficient at producing receptors from .alpha.7 gene constructs, although the same cells can produce receptors from other transfected gene constructs. The results indicate that nicotinic receptors that bind .alpha.-bungarotoxin and contain .alpha.7 subunits require additional gene products to facilitate assembly and stabilization of the receptors. PC12 cells offer a model system for identifying those gene products.

L137 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
ACCESSION NUMBER: 2002:72407 CAPLUS
DOCUMENT NUMBER: 136:131193
TITLE: Collections of binding proteins and tags and uses thereof for nested sorting and high throughput screening
INVENTOR(S): **Ault-Riche, Dana; Kassner, Paul D.**
PATENT ASSIGNEE(S): Pointilliste, Inc., USA
SOURCE: PCT Int. Appl., 160 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 2002006834 A2 20020124 WO 2001-US22821 20010718
WO 2002006834 C2 20020718
WO 2002006834 A3 20021010
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2002137053 A1 20020926 US 2001-910120 20010718
PRIORITY APPLN. INFO.: US 2000-219183P P 20000719

AB The invention concerns addressable collections of anti-tag capture agents, such as antibodies, that are used as tools for sorting proteins contain polypeptide tags for which the capture agents are specific. Also provided are methods of nested sorting using the collections. The methods includes the steps of creating tagged collections of mols. by introducing a set of nucleic acid mols. that encode unique preselected polypeptides to create a library of tagged mols.; either before or after introducing the tags, dividing the library into N divisions; translating each division and reacting each with one of N capture agent collections, identifying the capture agents bound to the polypeptide tags linked to mols. on interest, and thereby identifying the one of the divided collections that contains the mols. of interest. The method can further include adding a new set of tags and repeating the sorting process with the same or a different collection capture agents and thereby identifying a protein or mol. of interest.

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L4          9600 SEA FILE=CAPLUS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L5          9899 SEA FILE=CAPLUS ABB=ON  LIBRARY/CW
L6         23093 SEA FILE=CAPLUS ABB=ON  PROTEINS/CW(L)ANT/RL
L7         15667 SEA FILE=CAPLUS ABB=ON  ANTIBODIES/CW(L)ARG/RL
L9         81012 SEA FILE=CAPLUS ABB=ON  NUCLEIC ACID#/CW
L10       281822 SEA FILE=CAPLUS ABB=ON  (NUCLEOTIDE# OR OLIGONUCLEOTIDE#)/OBI
L11          741 SEA FILE=CAPLUS ABB=ON  L4 AND L9
L12         1056 SEA FILE=CAPLUS ABB=ON  L4 AND L10
L13            9 SEA FILE=CAPLUS ABB=ON  (L11 OR L12) AND L5 AND L6 AND L7
L14            9 SEA FILE=CAPLUS ABB=ON  L13 AND 9/SC,SX

L16           11 SEA FILE=CAPLUS ABB=ON  NEST?(2A)SORT?
L18            6 SEA FILE=CAPLUS ABB=ON  L16 NOT NESTIN
L19            4 SEA FILE=CAPLUS ABB=ON  L18 AND PCR


L4          9600 SEA FILE=CAPLUS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L5          9899 SEA FILE=CAPLUS ABB=ON  LIBRARY/CW
L6         23093 SEA FILE=CAPLUS ABB=ON  PROTEINS/CW(L)ANT/RL
L10       281822 SEA FILE=CAPLUS ABB=ON  (NUCLEOTIDE# OR OLIGONUCLEOTIDE#)/OBI
L21        11104 SEA FILE=CAPLUS ABB=ON  TAG####/OBI
L23           74 SEA FILE=CAPLUS ABB=ON  L4 AND L21 AND L5
L24           53 SEA FILE=CAPLUS ABB=ON  L10 AND L23
L25            4 SEA FILE=CAPLUS ABB=ON  L6 AND L24

=> s (l14 or l19 or l25) not l3
L138          14 (L14 OR L19 OR L25) NOT L3

=> fil wpids; d que l30; d que l39; d que l42; d que l45
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text search

ANT = analyte

ARG = analytical reagent use

Section code 9 = Biochemical Methods

previously printed

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L29             5 SEA FILE=WPIDS ABB=ON  NEST?(2A)SORT?
L30             1 SEA FILE=WPIDS ABB=ON  L29 AND LIBRAR?



L31         19302 SEA FILE=WPIDS ABB=ON  TAG####
L32         48577 SEA FILE=WPIDS ABB=ON  ANTIBOD?
L33         12636 SEA FILE=WPIDS ABB=ON  LIBRAR?
L34         53403 SEA FILE=WPIDS ABB=ON  NUCLEIC ACID# OR ?NUCLEOTIDE?
L35           184 SEA FILE=WPIDS ABB=ON  CAPTURE AGENT#
L36        103626 SEA FILE=WPIDS ABB=ON  PROTEIN#
L39             2 SEA FILE=WPIDS ABB=ON  L36 AND L32 AND (L31 AND L35) AND L33
                  AND L34



L31         19302 SEA FILE=WPIDS ABB=ON  TAG####
L32         48577 SEA FILE=WPIDS ABB=ON  ANTIBOD?
L33         12636 SEA FILE=WPIDS ABB=ON  LIBRAR?
L34         53403 SEA FILE=WPIDS ABB=ON  NUCLEIC ACID# OR ?NUCLEOTIDE?
L35           184 SEA FILE=WPIDS ABB=ON  CAPTURE AGENT#
L36        103626 SEA FILE=WPIDS ABB=ON  PROTEIN#
L40            89 SEA FILE=WPIDS ABB=ON  L36(S)L32(S)(L31 OR L35)(S)L33(S)L34
L41          4285 SEA FILE=WPIDS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L42            10 SEA FILE=WPIDS ABB=ON  L40 AND L41



L31         19302 SEA FILE=WPIDS ABB=ON  TAG####
L32         48577 SEA FILE=WPIDS ABB=ON  ANTIBOD?
L33         12636 SEA FILE=WPIDS ABB=ON  LIBRAR?
L34         53403 SEA FILE=WPIDS ABB=ON  NUCLEIC ACID# OR ?NUCLEOTIDE?
L35           184 SEA FILE=WPIDS ABB=ON  CAPTURE AGENT#
L36        103626 SEA FILE=WPIDS ABB=ON  PROTEIN#
L38           316 SEA FILE=WPIDS ABB=ON  L36 AND L32 AND (L31 OR L35) AND L33
                  AND L34
L43         13529 SEA FILE=WPIDS ABB=ON  NEST? NOT NESTIN
L45             3 SEA FILE=WPIDS ABB=ON  L38 AND L43


=> s (l30 or l39 or l42 or l45) not l28
L139           13 (L30 OR L39 OR L42 OR L45) NOT L28
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previously printed

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=> fil jic; d que l62; d que l63
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L52        3783 SEA FILE=JICST-EPLUS ABB=ON  NEST?
L54       21833 SEA FILE=JICST-EPLUS ABB=ON  PCR OR POLYMERASE CHAIN
L56         403 SEA FILE=JICST-EPLUS ABB=ON  L52(3A)L54
L57      243796 SEA FILE=JICST-EPLUS ABB=ON  PROTEIN#
L58       13469 SEA FILE=JICST-EPLUS ABB=ON  LIBRAR?
L62           2 SEA FILE=JICST-EPLUS ABB=ON  L56 AND L57 AND L58



L50         781 SEA FILE=JICST-EPLUS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH
                PUT)
L52        3783 SEA FILE=JICST-EPLUS ABB=ON  NEST?
L54       21833 SEA FILE=JICST-EPLUS ABB=ON  PCR OR POLYMERASE CHAIN
L56         403 SEA FILE=JICST-EPLUS ABB=ON  L52(3A)L54
L63           1 SEA FILE=JICST-EPLUS ABB=ON  L50 AND L56


=> s l62 or l63
L140          3 L62 OR L63

=> fil biosis; d que l83; d que l87; d que l88
FILE 'BIOSIS' ENTERED AT 11:44:33 ON 09 DEC 2002
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FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 4 December 2002 (20021204/ED)



L69        4194 SEA FILE=BIOSIS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L70       44419 SEA FILE=BIOSIS ABB=ON  LIBRAR?
L71       47285 SEA FILE=BIOSIS ABB=ON  NEST###
L72     1448418 SEA FILE=BIOSIS ABB=ON  PROTEIN#
L81      171699 SEA FILE=BIOSIS ABB=ON  PCR OR POLYMERASE CHAIN
L82        4385 SEA FILE=BIOSIS ABB=ON  L71(3A)L81
L83           1 SEA FILE=BIOSIS ABB=ON  L69 AND L70 AND L72 AND L82



L69        4194 SEA FILE=BIOSIS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L70       44419 SEA FILE=BIOSIS ABB=ON  LIBRAR?
L71       47285 SEA FILE=BIOSIS ABB=ON  NEST###
L72     1448418 SEA FILE=BIOSIS ABB=ON  PROTEIN#
L73      273621 SEA FILE=BIOSIS ABB=ON  ?NUCLEOTIDE?
L79      520371 SEA FILE=BIOSIS ABB=ON  ANTIBOD?
L81      171699 SEA FILE=BIOSIS ABB=ON  PCR OR POLYMERASE CHAIN
L82        4385 SEA FILE=BIOSIS ABB=ON  L71(3A)L81
L84          37 SEA FILE=BIOSIS ABB=ON  L72 AND L82 AND (L69 OR L70)
L85          18 SEA FILE=BIOSIS ABB=ON  L73 AND L84
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L87          2 SEA FILE=BIOSIS ABB=ON  L85 AND L79


L69       4194 SEA FILE=BIOSIS ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L70      44419 SEA FILE=BIOSIS ABB=ON  LIBRAR?
L71      47285 SEA FILE=BIOSIS ABB=ON  NEST###
L72    1448418 SEA FILE=BIOSIS ABB=ON  PROTEIN#
L74      28515 SEA FILE=BIOSIS ABB=ON  TAG####
L75        200 SEA FILE=BIOSIS ABB=ON  CAPTUR?(2A)AGENT#
L81     171699 SEA FILE=BIOSIS ABB=ON  PCR OR POLYMERASE CHAIN
L82       4385 SEA FILE=BIOSIS ABB=ON  L71(3A)L81
L84         37 SEA FILE=BIOSIS ABB=ON  L72 AND L82 AND (L69 OR L70)
L88          1 SEA FILE=BIOSIS ABB=ON  L84 AND (L74 OR L75)


=> s (l83 or l87 or l88) not l78
L141         4 (L83 OR L87 OR L88) NOT L78

=> fil medl; d que l96; d que l103; d que l109
FILE 'MEDLINE' ENTERED AT 11:44:36 ON 09 DEC 2002

 FILE LAST UPDATED: 23 NOV 2002 (20021123/UP). FILE COVERS 1958 TO DATE.

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 substance identification.


L95      13798 SEA FILE=MEDLINE ABB=ON  NEST###
L96          0 SEA FILE=MEDLINE ABB=ON  L95(W)SORT?


L92       3435 SEA FILE=MEDLINE ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L95      13798 SEA FILE=MEDLINE ABB=ON  NEST###
L97     554614 SEA FILE=MEDLINE ABB=ON  D12.776./CT(L)(AN OR CH OR DU)/CT
L102    128198 SEA FILE=MEDLINE ABB=ON  POLYMERASE CHAIN REACTION+NT/CT
L103         1 SEA FILE=MEDLINE ABB=ON  L97 AND L92 AND L95 AND L102


L92       3435 SEA FILE=MEDLINE ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)
L94      54544 SEA FILE=MEDLINE ABB=ON  LIBRAR?
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Proteins (l) Subheadings
AN - analysis
CH - chemistry
DU - diagnostic use

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L97       554614 SEA FILE=MEDLINE ABB=ON  D12.776./CT(L)(AN OR CH OR DU)/CT
L98       475964 SEA FILE=MEDLINE ABB=ON  D24.611.125./CT = antibodies
L100      119635 SEA FILE=MEDLINE ABB=ON  NUCLEIC ACID PROBES+NT/CT
L101       80968 SEA FILE=MEDLINE ABB=ON  OLIGONUCLEOTIDES+NT/CT
L102      128198 SEA FILE=MEDLINE ABB=ON  POLYMERASE CHAIN REACTION+NT/CT
L104      101480 SEA FILE=MEDLINE ABB=ON  L97 AND L98
L105       21276 SEA FILE=MEDLINE ABB=ON  TAG####
L106         487 SEA FILE=MEDLINE ABB=ON  L104 AND L105
L109           4 SEA FILE=MEDLINE ABB=ON  L106 AND (L94 OR L92) AND (L100 OR
                 L101) AND L102


=> s (l103 or l109) not l93
L142           5 (L103 OR L109) NOT L93  previously printed

=> fil biotechno; d que l123; d que l130;d que l132; d que l135; d que l136
FILE 'BIOTECHNO' ENTERED AT 11:44:39 ON 09 DEC 2002
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FILE LAST UPDATED: 3 DEC 2002       <20021203/UP>
FILE COVERS 1980 TO DATE.

>>>  SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN
     /CT AND BASIC INDEX  <<<


L121        6385 SEA FILE=BIOTECHNO ABB=ON  NEST###
L123           0 SEA FILE=BIOTECHNO ABB=ON  L121(2A)SORT? NOT NESTIN



L118      576528 SEA FILE=BIOTECHNO ABB=ON  PROTEIN#
L127          25 SEA FILE=BIOTECHNO ABB=ON  CAPTUR?(2A)AGENT#
L129        8306 SEA FILE=BIOTECHNO ABB=ON  DIAGNOSTIC VALUE/CT
L130           1 SEA FILE=BIOTECHNO ABB=ON  L118 AND L127 AND L129



L118      576528 SEA FILE=BIOTECHNO ABB=ON  PROTEIN#
L119      174323 SEA FILE=BIOTECHNO ABB=ON  NUCLEOTIDE# OR OLIGONUCLEOTIDE# OR
                 NUCLEIC ACID#
L120        2329 SEA FILE=BIOTECHNO ABB=ON  HIGH (W)(THROUGHPUT OR THROUGH PUT)

L121        6385 SEA FILE=BIOTECHNO ABB=ON  NEST###
L124      137590 SEA FILE=BIOTECHNO ABB=ON  POLYMERASE CHAIN OR PCR
L132           1 SEA FILE=BIOTECHNO ABB=ON  L118 AND L119 AND L121 AND L124 AND
                 L120



L117       33102 SEA FILE=BIOTECHNO ABB=ON  LIBRAR?
L118      576528 SEA FILE=BIOTECHNO ABB=ON  PROTEIN#
L119      174323 SEA FILE=BIOTECHNO ABB=ON  NUCLEOTIDE# OR OLIGONUCLEOTIDE# OR
                 NUCLEIC ACID#
L121        6385 SEA FILE=BIOTECHNO ABB=ON  NEST###
L124      137590 SEA FILE=BIOTECHNO ABB=ON  POLYMERASE CHAIN OR PCR
L125      200447 SEA FILE=BIOTECHNO ABB=ON  ANTIBOD?
L135           3 SEA FILE=BIOTECHNO ABB=ON  L118 AND L119 AND L121 AND L124 AND
                 L125 AND L117



L118      576528 SEA FILE=BIOTECHNO ABB=ON  PROTEIN#
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L119     174323 SEA FILE=BIOTECHNO ABB=ON  NUCLEOTIDE# OR OLIGONUCLEOTIDE# OR
                NUCLEIC ACID#
L121       6385 SEA FILE=BIOTECHNO ABB=ON  NEST###
L124     137590 SEA FILE=BIOTECHNO ABB=ON  POLYMERASE CHAIN OR PCR
L126      12969 SEA FILE=BIOTECHNO ABB=ON  TAG####
L136          3 SEA FILE=BIOTECHNO ABB=ON  L118 AND L119 AND L121 AND L124 AND
                L126


=> s (l130 or l132 or l135 or l136) not l114
L143          8 (L130 OR L132 OR L135 OR L136) NOT L114

=> dup rem l142,l140,l138,l141,l143,l139
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PROCESSING COMPLETED FOR L142
PROCESSING COMPLETED FOR L140
PROCESSING COMPLETED FOR L138
PROCESSING COMPLETED FOR L141
PROCESSING COMPLETED FOR L143
PROCESSING COMPLETED FOR L139
L144         45 DUP REM L142 L140 L138 L141 L143 L139 (2 DUPLICATES REMOVED)
                ANSWERS '1-5' FROM FILE MEDLINE
                ANSWERS '6-8' FROM FILE JICST-EPLUS
                ANSWERS '9-22' FROM FILE CAPLUS
                ANSWERS '23-26' FROM FILE BIOSIS
                ANSWERS '27-32' FROM FILE BIOTECHNO
                ANSWERS '33-45' FROM FILE WPIDS

=> d ibib ab 1-45;fil hom

L144 ANSWER 1 OF 45     MEDLINE
ACCESSION NUMBER:   2001226816     MEDLINE
DOCUMENT NUMBER:    21143360   PubMed ID: 11149944
TITLE:              Serological detection of cutaneous T-cell
                    lymphoma-associated antigens.
AUTHOR:             Eichmuller S; Usener D; Dummer R; Stein A; Thiel D;
                    Schadendorf D
CORPORATE SOURCE:   German Cancer Research Center (DKFZ), Skin Cancer Unit
                    (D0900), Im Neuenheimer Feld 280, D-69120 Heidelberg,
                    Germany.
SOURCE:             PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
                    UNITED STATES OF AMERICA, (2001 Jan 16) 98 (2) 629-34.
                    Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY:       United States
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
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previously printed

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF177227; GENBANK-AF177228; GENBANK-AF177229; GENBANK-AF273042; GENBANK-AF273043; GENBANK-AF273044; GENBANK-AF273045; GENBANK-AF273046; GENBANK-AF273047; GENBANK-AF273048; GENBANK-AF273049; GENBANK-AF273050; GENBANK-AF273051; GENBANK-AF273052; GENBANK-AF273053
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426

AB Cutaneous T-cell lymphomas (CTCL) are a group of skin neoplasms that originate from T lymphocytes and are difficult to treat in advanced stages. The present study is aimed at the identification of tumor-specific antigens from a human testis cDNA **library** using human sera known as the SEREX (serological identification of recombinantly expressed genes) approach. A cDNA **library** from normal testicle tissue was prepared and approximately 2 million recombinants were screened with sera from Sezary Syndrome and Mycosis fungoides patients. A total of 28 positive clones belonging to 15 different genes/ORFs were identified, including five hitherto unknown sequences. Whereas control sera did not react with most clones, 11-71% sera from CTCL patients were reactive against the identified clones. Expression analysis on 28 normal control and 17 CTCL tissues by reverse transcription-PCR (RT-PCR) and Northern blotting revealed seven ubiquitously distributed antigens, six differentially expressed antigens (several normal tissues were positive), and two tumor-specific antigens that were expressed only in testis and tumor tissues: (i) A SCP-1-like sequence, which has already been detected in various tumors, has been found in one CTCL tumor and four sera of CTCL patients reacted with various SCP-1-like clones and (ii) a new sequence named cTAGE-1 (CTCL-associated antigen 1) was detected in 35% of CTCL tumor tissues and sera of 6/18 patients reacted with this clone. The present study unravels CTCL-associated antigens independent of the T-cell receptor. The SCP-1-like gene and cTAGE-1 were shown to be immunogenic and immunologically tumor-specific and may therefore be candidates for immunotherapy targeting CTCL.

L144 ANSWER 2 OF 45 MEDLINE
ACCESSION NUMBER: 2000396495 MEDLINE
DOCUMENT NUMBER: 20317114 PubMed ID: 10779521
TITLE: Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.
AUTHOR: Palmeri D; van Zante A; Huang C C; Hemmerich S; Rosen S D
CORPORATE SOURCE: Department of Anatomy and the Cardiovascular Research Institute, the Program in Immunology, University of California, USA.
CONTRACT NUMBER: R37GM23547 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Jun 23) 275 (25) 19139-45.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF255910; GENBANK-AF255911
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000816

AB During the process of lymphocyte homing to secondary lymphoid organs, such as lymph nodes and tonsils, lymphocytes interact with and cross a specialized microvasculature, known as high endothelial venules. There is a great deal of information available about the first steps in the homing

cascade, but molecular understanding of lymphocyte transmigration through the intercellular junctions of high endothelial venules is lacking. In analyzing expressed sequence **tags** from a cDNA **library** prepared from human tonsillar high endothelial cells, we have identified a cDNA encoding a novel member of the immunoglobulin superfamily. The protein, which we have termed VE-JAM ("vascular endothelial junction-associated molecule"), contains two extracellular immunoglobulin-like domains, a transmembrane domain, and a relatively short cytoplasmic tail. VE-JAM is prominently expressed on high endothelial venules but is also present on the endothelia of other vessels. Strikingly, it is highly localized to the intercellular boundaries of high endothelial cells. VE-JAM is most homologous to a recently identified molecule known as Junctional Adhesion Molecule, which is concentrated at the intercellular boundaries of both epithelial and endothelial cells. Because the Junctional Adhesion Molecule has been strongly implicated in the processes of neutrophil and monocyte transendothelial migration, an analogous function of VE-JAM during lymphocyte homing is plausible.

L144 ANSWER 3 OF 45 MEDLINE
ACCESSION NUMBER: 1999436254 MEDLINE
DOCUMENT NUMBER: 99436254 PubMed ID: 10504458
TITLE: Comparative mutation detection screening of the type VII collagen gene (COL7A1) using the protein truncation test, fluorescent chemical cleavage of mismatch, and conformation sensitive gel electrophoresis.
AUTHOR: Whittock N V; Ashton G H; Mohammedi R; Mellerio J E; Mathew C G; Abbs S J; Eady R A; McGrath J A
CORPORATE SOURCE: Department of Cell and Molecular Pathology, St John's Institute of Dermatology, St Thomas' Hospitals' Medical School, London, UK.. neil.whittock@kcl.ac.uk
SOURCE: JOURNAL OF INVESTIGATIVE DERMATOLOGY, (1999 Oct) 113 (4) 673-86.
Journal code: 0426720. ISSN: 0022-202X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991104

AB Mutations in the type VII collagen gene, COL7A1, give rise to the blistering skin disease, dystrophic epidermolysis bullosa. We have developed two new mutation detection strategies for the screening of COL7A1 mutations in patients with dystrophic epidermolysis bullosa and compared them with an established protocol using conformational sensitive gel electrophoresis. The first strategy consisted of an RNA based protein truncation test that amplified the entire coding region in only four overlapping **nested** reverse transcriptase-polymerase chain reaction assays. These fragments were transcribed and translated in vitro and analyzed using sodium dodecyl sulfate-polyacrylamide gel electrophoresis. We have used the protein truncation test procedure to characterize 15 truncating mutations in 13 patients with severe recessive dystrophic epidermolysis bullosa yielding a detection sensitivity of 58%. The second strategy was a DNA-based fluorescent chemical cleavage of mismatch (fl-CCM) procedure that amplified the COL7A1 gene in 21 polymerase chain reaction assays. Mismatches, formed between patient and control DNA, were identified using chemical modification and cleavage of the DNA. We have compared fl-CCM with conformational sensitive gel electrophoresis by screening a total of 50 dominant and recessive dystrophic epidermolysis bullosa patients. The detection sensitivity for fl-CCM was 81% compared with 75% for conformational sensitive gel

electrophoresis (p = 0.37 chi2-test). Using a combination of the three techniques we have screened 93 dystrophic epidermolysis bullosa patients yielding an overall sensitivity of 87%, detecting 79 different mutations, 57 of which have not been reported previously. Comparing all three approaches, we believe that no single method is consistently better than the others, but that the fl-CCM procedure is a sensitive, semiautomated, **high throughput** system that can be recommended for COL7A1 mutation detection.

L144 ANSWER 4 OF 45 MEDLINE
ACCESSION NUMBER: 1999142307 MEDLINE
DOCUMENT NUMBER: 99142307 PubMed ID: 9987819
TITLE: Cloning and expression of a gene encoding a Campoletis sonorensis polydnavirus structural protein.
AUTHOR: Deng L; Webb B A
CORPORATE SOURCE: Dept. of Entomology, University of Kentucky, Lexington 40546-0091, USA.
SOURCE: ARCHIVES OF INSECT BIOCHEMISTRY AND PHYSIOLOGY, (1999) 40 (1) 30-40.
Journal code: 8501752. ISSN: 0739-4462.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF004367
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 19990316
Entered Medline: 19990304

AB Polydnaviruses are the only known group of mutualistic viruses. They are required for successful parasitization in many braconid and ichneumonid parasitoids. The intimacy of this mutualistic association is indicated by the integration and vertical transmission of polydnaviruses in wasp genomes and by their asymptomatic, developmentally regulated replication. The evolution of this mutualism raises several interesting issues that require a better understanding of the viral genome and viral replication. To develop probes for virus replication and morphogenesis, we have begun to characterize several viral structural proteins. A 699 bp cDNA encoding the p12 viral structural protein was cloned and sequenced. The p12 gene localizes to viral segment Y and encodes a predicted protein of 92 amino acids that does not encode a signal peptide and is unrelated to known peptide or nucleic acid sequences. The p12 mRNA is detected at the onset of virus replication. mRNA titers increase with increasing rates of virus replication. Polyclonal antisera raised against histidine-**tagged** p12 protein expressed in bacteria reacted specifically with the p12 polypeptide in Western blots of CsPDV virions. The p12 polypeptide was not detected in non-replicative wasp or lepidopteran tissues by Western blot analyses but was readily detected in protein extracts of wasp ovaries. The data indicate that the p12 gene is a viral gene encoding a virion protein and provides a specific probe for virus replication that will be useful for studying the evolution of this group of mutualistic viruses.

L144 ANSWER 5 OF 45 MEDLINE
ACCESSION NUMBER: 97183046 MEDLINE
DOCUMENT NUMBER: 97183046 PubMed ID: 9116854
TITLE: Signal sequence trap. Expression cloning method for secreted proteins and type 1 membrane proteins.
AUTHOR: Tashiro K; Nakano T; Honjo T
CORPORATE SOURCE: Department of Medical Chemistry, Faculty of Medicine, Kyoto University, Japan.
SOURCE: METHODS IN MOLECULAR BIOLOGY, (1997) 69 203-19.
Journal code: 9214969. ISSN: 1064-3745.
PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970506
Last Updated on STN: 19970506
Entered Medline: 19970424

L144 ANSWER 6 OF 45 JICST-EPlus COPYRIGHT 2002 JST
ACCESSION NUMBER: 1010818748 JICST-EPlus
TITLE: **High-throughput** HTLV-1 proviral DNA detection system using a nucleic acid extraction robot and real-time PCR detection.
AUTHOR: MATSUMOTO CHIEKO; SHIOZAWA RIEKO; MITSUNAGA SHIGEKI; ICHIKAWA AKIKO; ISHIWATARI RIKA; UCHIDA SHIGEHARU; NAKAJIMA KAZUNORI; TADOKORO KENJI; JUJI TAKEO
CORPORATE SOURCE: Japan Red Cross Soc. Cent. Blood Center
SOURCE: Nippon Yuketsu Gakkai Zasshi (Journal of the Japan Society of Blood Transfusion), (2001) vol. 47, no. 3, pp. 378-383.
Journal Code: Z0301B (Fig. 1, Tbl. 3, Ref. 11)
ISSN: 0546-1448
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
LANGUAGE: Japanese
STATUS: New
AB A **high-throughput** nucleic acid testing system was developed for detecting proviral DNA of human T-cell leukemia virus type 1 (HTLV-1), using an automatic nucleic acid extractor and the real-time detection TaqMan PCR (TaqMan PCR) targeting the pX region of the HTLV-1 genome. Approximately 4 .MU.g and 2.5 .MU.g of DNA were obtained from 200 .MU.l of whole blood and 100 .MU.l of frozen blood cells separated from whole blood, respectively. Extraction of nucleic acid from 48 blood samples was completed within 120 minutes. The detection limit of the TaqMan PCR was as high as that of the **nested PCR**. Amplification and detection of HTLV-1 genome in 96 blood samples was completed within 160 minutes. Extraction plus TaqMan PCR for viral genome as well as enzyme immunoassay (EIA) and indirect immunofluorescence assay (IF) for HTLV-1-antibodies were performed to test 38 blood samples which were determined to be HTLV-1-antibody positive by the donor screening test using particle agglutination. The results of EIA and IF coincided well with those of the TaqMan PCR, indicating that this detection system for HTLV-1 provirus DNA was useful for testing many samples in a short time with high sensitivity and specificity. (author abst.)

L144 ANSWER 7 OF 45 JICST-EPlus COPYRIGHT 2002 JST
ACCESSION NUMBER: 1001054322 JICST-EPlus
TITLE: Single-Step Single-Molecule PCR of DNA with a Homo-Priming Sequence Using a Single Primer and Hot-Startable DNA Polymerase.
AUTHOR: NAKANO H; KOBAYASHI K; OHUCHI S; YAMANE T
SEKIGUCHI S
CORPORATE SOURCE: Nagoya Univ., Nagoya, Jpn
Nippon Flour Mills Co. Ltd., Kanagawa, Jpn
SOURCE: J Biosci Bioeng, (2000) vol. 90, no. 4, pp. 456-458.
Journal Code: G0535B (Fig. 1, Tbl. 1, Ref. 13)
ISSN: 1389-1723
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
LANGUAGE: English
STATUS: New
AB We have previously reported that a **protein library** can be constructed by directly combining PCR amplification of a single DNA molecule and cell-free **protein** synthesis. To specifically

amplify single DNA molecules, however, two-step PCR with **nested** primers was used. Here we describe a simpler method for single-step amplification of a single molecule. The method involves the use of both hot-startable DNA polymerase and a DNA template that has homo-priming sequences at both ends for amplification using a single primer. These two modifications greatly decreased the possibility of formation and subsequent accumulation, respectively, of primer-dimers that inhibit the amplification of target template. In addition, a high-fidelity DNA polymerase was successfully used, resulting in the significant reduction of the accumulation of mutations during amplification. (author abst.)

L144 ANSWER 8 OF 45 JICST-EPlus COPYRIGHT 2002 JST
ACCESSION NUMBER: 1000559825 JICST-EPlus
TITLE: Molecular Cloning and Characterization of a Subfamily of UV-B Responsive MYB genes from Soybean.
AUTHOR: SHIMIZU T; FUJIBE R; SENDA M; ISHIKAWA R; HARADA T; NIIZEKI M; AKADA S
CORPORATE SOURCE: Hirosaki Univ., Aomori, Jpn
SOURCE: Breed Sci, (2000) vol. 50, no. 2, pp. 81-90. Journal Code: Y0311B (Fig. 6, Tbl. 1, Ref. 27)
ISSN: 1344-7610
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
LANGUAGE: English
STATUS: New

AB Flavonoid compounds accumulating in the epidermal cell layers of plant tissues are considered to be among the most effective protectants against the ultraviolet-B (UV-B) radiation. To identify a transcription factor involved in the activation of the genes, such as chalcone synthase genes (CHS), in the pathway of flavonoid biosynthesis, a pair of degenerate primers was designed to amplify the most conservative region of MYB from soybean by polymerase chain reaction (PCR) or reverse transcriptase (RT)-PCR. Both of these amplification products were found to contain molecules of dozens of independent MYB-like sequences. The bacterial clones harboring a partial **library** of the RT-PCR products were differentially hybridized with the amplified cDNA fragments derived from total RNA of UV-B treated seedlings (rMYB/UV-B+) and those from control RNA (rMYB/UV-B-). One clone designated as MYB29 showed a significantly stronger signal with rMYB /UV-B+ hybridization than with rMYB /UV-B-. Starting from the sequence information of MYB29 fragment, an entire sequence containing the complete gene designated as GmMYB29A1 was obtained by **nested PCR** of the flanking regions. In the course of this PCR cloning, we identified several independent products closely related to GmMYB29A1. In order to amplify the entire **protein** coding region of the closely related genes, two sets of primers were designed, two up-stream primers containing the ATG start codon and the other two downstream primers containing the TGA stop codon. By sequencing those cDNAs amplified with RT-PCR, a total of at least four members were found to comprise the subfamily, designated as GmMYB29. UV-B-responsive expression of the members of GmMYB29 was found to reach its peak within 2 hours after the onset of light exposure while in those of soybean (Gm)CHS it continued to rise for 6 hours.... (author abst.)

L144 ANSWER 9 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:814163 CAPLUS
DOCUMENT NUMBER: 137:322269
TITLE: Selective covalent-binding compounds having therapeutic, diagnostic and analytical applications
INVENTOR(S): Green, Bernard S.
PATENT ASSIGNEE(S): Semorex Inc., USA
SOURCE: PCT Int. Appl., 67 pp.
CODEN: PIXXD2

Searched by Barb O'Bryen, STIC 308-4291

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002083708	A2	20021024	WO 2002-IL307	20020416

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-283645P P 20010416

AB Novel compds. are provided having enhanced affinity for a desired, preselected, target substance (a small mol.; a macromol. such as a protein, a carbohydrate, a nucleic acid, a cell, a viral particle, etc.) by modification with chem. groups that allow these substances to form strong bonds, such as irreversible covalent bonds, with the desired target substance. These qualities of tight, specific binding are reminiscent of antibody-like affinity; hence the new substances are termed COBALT, an acronym for covalent-binding antibody-like trap. The present invention includes a process wherein a target species is chosen and then, by synthetic chem. procedures and modifications, novel substances (COBALTs) are obtained that exhibit selective and covalent binding to the preselected target species. The applications of the COBALTs include diagnostic, anal., therapeutic and industrial applications. Cholesterol-binding molecularly-imprinted polymer MS50 was prepd. by polymn. of cholesteryl (4-vinyl)phenyl carbamate (template monomer), EGDM and cholesteryl methacrylate to make polymer MS41 and subsequent removal of the cholesterol from the carbamate in polymer MS41. COBALTs MS71 and MS80 were made by reaction of MS50 with triphosgene and thiophosgene, resp., for better cholesterol binding activity.

L144 ANSWER 10 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:595050 CAPLUS
DOCUMENT NUMBER: 137:137215
TITLE: Biochip device and methods for **oligonucleotide** identification
INVENTOR(S): Bamdad, Cynthia Carol; Bambad, R. Shoshana
PATENT ASSIGNEE(S): Minerva Biotechnologies Corporation, USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002061129	A2	20020808	WO 2001-US45845	20011115

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,

CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2002164611 A1 20021107 US 2001-4275 20011115
PRIORITY APPLN. INFO.: US 2000-248863P P 20001115
US 2000-252650P P 20001122
GB 2001-1054 A 20010115
US 2001-276995P P 20010319
US 2001-302231P P 20010629
US 2001-326937P P 20011003
US 2001-327089P P 20011003

AB The invention concerns methods, assays, and components in which biol. samples can be rapidly and sensitively analyzed for the presence of species assocd. with neurodegenerative disease. Techniques and components are provided for diagnosis of disease, as well as for screening of candidate drugs for treatment of neurodegenerative disease. The techniques are simple, extremely sensitive, and utilize readily-available components. Binding species, capable of binding a neurodegenerative disease aggregate-forming or aggregate-forming species, are fastened to surfaces of electrodes and surfaces of particles, or provided free in soln., to bind aggregate-forming species and/or be involved in aggregation. Diagrams describing the app. and its assembly are given.

L144 ANSWER 11 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:466235 CAPLUS
DOCUMENT NUMBER: 137:17414
TITLE: System for multiplexed protein expression and activity assay
INVENTOR(S): Monforte, Joseph A.
PATENT ASSIGNEE(S): HK Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 67 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002048403	A2	20020620	WO 2001-US48023	20011211

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002030788 A5 20020624 AU 2002-30788 20011211
PRIORITY APPLN. INFO.: US 2000-254958P P 20001211
WO 2001-US48023 W 20011211

AB The invention concerns a system for analyzing expression levels and activity of a plurality of proteins. A bio-displayed polypeptide binding component assocd. with a predetd. marker is used to bind the proteins of interest. The predetd. marker components are then amplified and detected in a **high throughput** manner.

L144 ANSWER 12 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:332318 CAPLUS
DOCUMENT NUMBER: 136:337348
TITLE: Isolation of binding proteins with high affinity to ligands

Searched by Barb O'Bryen, STIC 308-4291

INVENTOR(S): Chen, Gang; Hayhurst, Andrew; Thomas, Jeffrey G.; Iverson, Brent L.; Georgiou, George
PATENT ASSIGNEE(S): Board of Regents, the University of Texas System, USA
SOURCE: PCT Int. Appl., 98 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002034886	A2	20020502	WO 2001-US46795	20011026
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002030635	A5	20020506	AU 2002-30635	20011026

PRIORITY APPLN. INFO.: US 2000-699023 A 20001027
WO 2001-US46795 W 20011026

AB The invention overcomes the deficiencies of the prior art by providing a rapid approach for isolating binding proteins capable of binding small mols. and peptides via "display-less" library screening. In the technique, libraries of candidate binding proteins, such as antibody sequences, are expressed in sol. form in the periplasmic space of gram neg. bacteria, such as Escherichia coli, and are mixed with a labeled ligand. In clones expressing recombinant polypeptides with affinity for the ligand, the concn. of the labeled ligand bound to the binding protein is increased and allows the cells to be isolated from the rest of the library. Where fluorescent labeling of the target ligand is used, cells may be isolated by fluorescence activated cell sorting (FACS). The approach is more rapid than prior art methods and avoids problems assocd. with the surface-expression of ligand fusion proteins employed with phage display.

L144 ANSWER 13 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:256769 CAPLUS
DOCUMENT NUMBER: 136:258374
TITLE: Human breast and ovarian-cancer-associated gene sequences and polypeptides
INVENTOR(S): Rosen, Craig A.; Ruben, Steven M.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 199 pp., Cont.-in-part of Appl. No. PCT/US2000/05881.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 10
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002039764	A1	20020404	US 2001-925298	20010810
WO 2000055173	A1	20000921	WO 2000-US5881	20000308
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				

RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-124270P P 19990312
WO 2000-US5881 A2 20000308

AB The present invention relates to novel ovarian cancer and/or breast cancer-related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "ovarian and/or breast antigens," and antibodies that immunospecifically bind these polypeptides, and the use of such ovarian and/or breast polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the reproductive system, particularly disorders of the ovaries and/or breast, including, but not limited to, the presence of ovarian and/or breast cancer and ovarian and/or breast cancer metastases. More specifically, 418 isolated ovarian and/or breast cDNA acid mols. are provided encoding novel ovarian and/or breast polypeptides that are expressed at significantly enhanced levels in human breast, ovarian, breast cancer, and/or ovarian cancer tissues. Novel ovarian and/or breast polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human ovarian and/or breast polynucleotides, polypeptides, and/or antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the ovaries and/or breast, including ovarian and/or breast cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compns. for inhibiting or promoting the prodn. and/or function of the polypeptides of the invention.

L144 ANSWER 14 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:904740 CAPLUS
DOCUMENT NUMBER: 136:17685
TITLE: Screening of phage displayed peptides without clearing of the cell culture
INVENTOR(S): Nock, Steffen; Kassner, Paul D.
PATENT ASSIGNEE(S): Zyomyx, Inc., USA
SOURCE: PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001094950	A2	20011213	WO 2001-US18421	20010605
WO 2001094950	A3	20020510		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2002058269 A1 20020516 US 2001-874547 20010604

PRIORITY APPLN. INFO.: US 2000-209503P P 20000605
US 2001-874547 A 20010604

AB The invention concerns methods for screening populations of phage-displayed polypeptides that are particularly well-suited for

high-throughput screening. The methods do not require the clearing of cells from a culture used to obtain the population of phage or other replicable genetic packages. Accordingly, the invention provides methods for forming complexes between a replicable genetic package displaying a polypeptide fusion and a target mol. in an uncleared cell culture contg. replicable genetic package. Compns. made up of an uncleared cell culture contg. replicable genetic packages displaying a polypeptide fusion and a target mol. are provided in the invention as well.

L144 ANSWER 15 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:781183 CAPLUS
DOCUMENT NUMBER: 135:328960
TITLE: Library screening system to detect protein-protein interactions
INVENTOR(S): Lilien, Jack; Elferink, Lisa A.; Balsamo, Janne; Kamholz, John
PATENT ASSIGNEE(S): Wayne State University, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001079559	A1	20011025	WO 2001-US12457	20010418
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002081570	A1	20020627	US 2001-836865	20010418

PRIORITY APPLN. INFO.: US 2000-198122P P 20000418
AB The invention concerns a method for screening protein-protein interactions that is rapid, easy and generally applicable to a wide array of such interactions is disclosed. This method, an adaptation and combination of certain existing approaches, uses T7 phage display libraries and target epitope arrays synthesized, for example, by simultaneous synthesis overlapping peptides of known sequences. These methods provide for **high throughput** screening that can identify the particular amino acids or domains or epitopes that are of primary importance in the binding interactions between two protein partners.
REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L144 ANSWER 16 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:748068 CAPLUS
DOCUMENT NUMBER: 135:314387
TITLE: Gene sorting and non-redundant cDNA library construction using sequence-specific adaptors
INVENTOR(S): Ulanovsky, Levy; Mugasimangalam, Raja; Einat, Paz; Zezin-sonkin, Dina; Shlomit, Gilad
PATENT ASSIGNEE(S): QBI Enterprises Ltd., Israel
SOURCE: PCT Int. Appl., 67 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001075180	A2	20011011	WO 2001-US9392	20010323
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
US 6468749	B1	20021022	US 2000-538709	20000330

PRIORITY APPLN. INFO.: US 2000-538709 A 20000330

AB The present invention discloses techniques for simply and efficiently sorting expressed genes into non-redundant groups of cDNA mols. reverse-transcribed from any source of eukaryotic RNA. This method comprises: (1) prepg. ds cDNA mols. from mRNA mols.; (2) digesting the ds cDNA mols.; (3) ligating to the digested cDNA mols. a set of dsDNA oligonucleotide adaptors; (4) amplifying the ligated cDNA mols.; and (5) sorting the amplified cDNA mols. into non-redundant groups. This invention also provides two addnl. methods of sorting genes. This invention further provides a method of making sub-libraries of ligation sets and a method of making sub-libraries of genetic vectors. The present invention provides novel methods for producing a non-redundant cDNA or gene library. The methods sort DNA on a sequence-dependent basis into non-redundant groups. At the same time, however, these methods eliminate the need to det. any of the DNA sequences prior to sorting and identifying genes. In the examples as shown in Figure 4, double stranded cDNA derived from rat liver mRNA was digested with BbvI and ligated to Tail adaptor set 2.

L144 ANSWER 17 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:618205 CAPLUS
DOCUMENT NUMBER: 135:191299
TITLE: Human vomeronasal organ cDNA libraries and proteins identified from the library
INVENTOR(S): Herman, Ronald C.; Berliner, David
PATENT ASSIGNEE(S): Pherin Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001061046	A2	20010823	WO 2001-US5178	20010215
WO 2001061046	A3	20020314		
W:	AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

US 2002155444 A1 20021024 US 2001-783252 20010213
PRIORITY APPLN. INFO.: US 2000-183128P P 20000217
AB This invention relates to DNA libraries, in particular a human vomeronasal organ (VNO) cDNA library. Pheromone receptor cDNA isolated is transfected into competent cells. The transfected cell lines provide a scalable source of homogeneous material to develop efficient, automated **high throughput** screening assays for new vomeropherins, and thereby reduce the ongoing need for human volunteers in the preclin. phases of drug discovery. Identification and characterization of the human VNO receptor(s) will facilitate the development and commercialization of vomeropherins with improved specificity, and enhanced therapeutic efficacy in the treatment of the target diseases. The invention provides methods to identify and isolate DNA encoding pheromone receptors.

L144 ANSWER 18 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:210502 CAPLUS
DOCUMENT NUMBER: 132:231929
TITLE: Method and apparatus for cell-based drug screening
INVENTOR(S): Dunlay, R. Terry; Taylor, D. Lansing; Gough, Albert H.; Guiliano, Kenneth A.; Rubin, Richard A.
PATENT ASSIGNEE(S): Cellomics, Inc., USA
SOURCE: PCT Int. Appl., 147 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000017643	A2	20000330	WO 1999-US21561	19990917
WO 2000017643	A3	20001012		
W: AU, CA, JP, MX, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2344567	AA	20000330	CA 1999-2344567	19990917
AU 9960485	A1	20000410	AU 1999-60485	19990917
EP 1114320	A2	20010711	EP 1999-969495	19990917
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002525603	T2	20020813	JP 2000-571253	19990917

PRIORITY APPLN. INFO.: US 1998-100973P P 19980918
WO 1999-US21561 W 19990917

AB The invention concerns a **high throughput** screening method to identify compds. that modify transcription factor activation and/or protein kinase activation by contacting cells that contain fluorescent labeled transcription factors/protein kinases with the test compd. and detecting the distribution of the labeled compd. between cell nucleus and cytoplasm using an automated analyzer. The present invention provides systems, methods, screens, and kits for optical system anal. of cells to rapidly det. the distribution, environment, or activity of fluorescently labeled reporter mols. in cells for the purpose of screening large nos. of compds. for those that specifically affect particular biol. functions. The invention involves providing cells contg. fluorescent reporter mols. in an array of locations and scanning numerous cells in each location with a high magnification fluorescence optical system, converting the optical information into digital data, and utilizing the digital data to det. the distribution, environment or activity of the fluorescently labeled reporter mols. in the cells. The array of locations may be an industry std. 96 well or 384 well microtiter plate or a microplate which is a microplate having cells in a micropatterned array of locations. The invention includes app. and computerized method for

processing, displaying and storing the data.

L144 ANSWER 19 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:905314 CAPLUS
DOCUMENT NUMBER: 135:221900
TITLE: Separation and enrichment of fetal nucleated red blood cells from maternal blood for non-invasive prenatal gene diagnosis
AUTHOR(S): Xie, Jiansheng; Long, Guifang
CORPORATE SOURCE: Department of Pediatrics, First Affiliated Hospital, Guangxi Medical University, Nanning, 530021, Peop. Rep. China
SOURCE: Zhonghua Xueyexue Zazhi (2000), 21(10), 512-516
CODEN: CHTCD7; ISSN: 0253-2727
PUBLISHER: Zhongguo Yixue Kexueyuan Xueyexue Yanjiuso
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB A non-invasive technique for prenatal gene diagnosis was presented. Peripheral blood mononuclear cells (MNCs) were sepd. by single d. gradient Histopaque 1.077 from 25 pregnant women with gestation between 8-36 w. The fetal nucleated red blood cells (NRBCs) were enriched from the MNCs by pos. selection using Dynabeads M-450 CD71 or neg. selection using Dynabeads M-450 CD45. The enriched NRBCs were identified by anti-.gamma.-biotin or anti-.zeta.-biotin antibodies. Globin gene of NRBCs from fetuses with risk of .beta.-thalassemia major were amplified by nested **PCR** followed by reverse dot blot hybridization for gene diagnosis. There were NRBCs stained by anti-.gamma.-biotin or anti-.zeta.-biotin antibodies in the peripheral blood samples of the 25 pregnant women. 3 Of 5 fetuses with risk of .beta.-thalassemia major were successfully diagnosed using the NRBCs. The results showed that fetal NRBCs in maternal circulation can be isolated and enriched by single gradient d. Histopaque 1.077 followed by magnetic activated cell **sorting**, and **nested PCR** can amplify DNA for gene diagnosis from no less than 20 NRBCs.

L144 ANSWER 20 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:577053 CAPLUS
DOCUMENT NUMBER: 131:181979
TITLE: **Tagged** ligand arrays for identifying ligand-target interactions
INVENTOR(S): Burmer, Glenna C.
PATENT ASSIGNEE(S): Lifespan Biosciences, Inc., USA
SOURCE: PCT Int. Appl., 33 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9945149	A1	19990910	WO 1999-US4378	19990226
W: AU, CA, JP, KR				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6087103	A	20000711	US 1998-34622	19980304
CA 2322788	AA	19990910	CA 1999-2322788	19990226
AU 9928833	A1	19990920	AU 1999-28833	19990226
EP 1071813	A1	20010131	EP 1999-909680	19990226
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002505119	T2	20020219	JP 2000-534680	19990226

PRIORITY APPLN. INFO.: US 1998-34622 A 19980304

WO 1999-US4378 W 19990226

AB The present invention relates generally to **high throughput** screening methods. More particularly, the present invention provides screening methods that can readily be used to identify simultaneously multiple proteins or compds. that interact with multiple ligands, using a tagged array of ligands.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L144 ANSWER 21 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:405112 CAPLUS
DOCUMENT NUMBER: 131:56155
TITLE: Methods for the simultaneous identification of novel biological targets and lead structures for drug development using combinatorial libraries and probes
INVENTOR(S): Heefner, Donald L.; Zepp, Charles M.; Gao, Yun; Jones, Steven W.
PATENT ASSIGNEE(S): Sepracor Inc., USA
SOURCE: PCT Int. Appl., 125 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9931267	A1	19990624	WO 1998-US26894	19981218
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2314422	AA	19990624	CA 1998-2314422	19981218
AU 9919256	A1	19990705	AU 1999-19256	19981218
EP 1049796	A1	20001108	EP 1998-964053	19981218
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002508507	T2	20020319	JP 2000-539165	19981218

PRIORITY APPLN. INFO.: US 1997-68035P P 19971218
WO 1998-US26894 W 19981218

AB The combinatorial screening assays and detection methods of the present invention encompass highly diversified libraries of compds. which act as fingerprints to allow for the identification of specific mol. differences existing between biol. samples. The combinatorial screening assay and detection methods of the present invention utilize highly diversified libraries of compds. to interrogate and characterize complex mixts. in order to identify specific mol. differences existing between biol. samples, which may serve as targets for diagnosis of development of therapeutics. The invention is base, in part, on the design of sensitive, rapid, homogeneous assay systems that permit the evaluation, interrogation, and characterization of samples using complex, highly diversified libraries of mol. probes. The ability to run the **high throughput** assays in a homogeneous format increases sensitivity of screening. In addn., the homogeneous format allows the mols. which interact to maintain their native or active conformations. Moreover, the homogeneous assay systems of the invention utilize robust detection systems that do not require sepn. steps for detection of reaction products. The assays of the invention can be used for diagnostics, drug screening and discovery, target-driven discover, and in the field of

proteomics and genomics for the identification of disease markers and drug targets.
REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L144 ANSWER 22 OF 45 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:642205 CAPLUS
DOCUMENT NUMBER: 129:272552
TITLE: Detection of fetal cells from maternal peripheral blood
AUTHOR(S): Moriai, Kayo; Fukushima, Akimune
CORPORATE SOURCE: Sch. Med., Iwate Med. Univ., Morioka, 020-8505, Japan
SOURCE: Iwate Igaku Zasshi (1998), 50(4), 429-438
CODEN: IIZAAX; ISSN: 0021-3284
PUBLISHER: Iwate Igakkai
DOCUMENT TYPE: Journal
LANGUAGE: Japanese
AB We attempted to det. fetal sex using maternal peripheral blood sampled from pregnant women. The purpose of this study is to bring this method into practical use for noninvasive prenatal diagnosis. Ten mL of peripheral blood was obtained from each women, and eukaryotic cells were promptly sepd. by gravity centrifugation. Then, cells neg. for CD45 monoclonal antibody (CD45) and pos. for glycophorin A monoclonal antibody (GA) were selectively collected using a magnetic activated cell sorting system (MACS) to obtain embryonic nucleated erythrocytes (NRBC). After DNA extn. from the collected cells, the nested **PCR** was performed. Fetuses were judged to be male when Y chromosomes were detected. Among Y chromosome-pos. cases, 92.9% were detd. to be male after birth. Among Y chromosome-neg. cases, 57.1% were detd. to be female after birth. False pos. and neg. rates, detd. by our method, were 7.1% and 42.9%, resp. Our method, combining the MACS and the nested **PCR**, provided a clue to obtain a simple and accurate approach for prenatal diagnosis. The further improvement of the current method through the redn. of false pos. and neg. rates indicates the possibility of its application to clin. cases.

L144 ANSWER 23 OF 45 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
ACCESSION NUMBER: 2001:102868 BIOSIS
DOCUMENT NUMBER: PREV200100102868
TITLE: Molecular cloning of a tumor-associated antigen recognized by monoclonal **antibody** 3H11.
AUTHOR(S): Chen, Donghai; Shou, Chengchao (1)
CORPORATE SOURCE: (1) Beijing Institute for Cancer Research and Beijing Cancer Hospital, Peking University School of Oncology, Beijing, 100034: cshou@sinanet.com China
SOURCE: Biochemical and Biophysical Research Communications, (January 12, 2001) Vol. 280, No. 1, pp. 99-103. print.
ISSN: 0006-291X.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Monoclonal **antibody** (MAb) 3H11 can bind specifically to different cancer cells from different tissues. MAb 3H11 labeled with radioactive isotopes has been used clinically to detect primary cancer and metastatic cancer. Molecular cloning of the antigen recognized by MAb 3H11 is important in studying tumor occurrence and in developing new biotherapy for cancer. Using MAb 3H11, we screened cDNA **library** made from the human gastric cancer cell line MGC 803, which reacts with MAb 3H11, and isolated one positive clone specifically recognized by the **antibody**. The insert cDNA fragment was 0.5 kb. After recombining with glutathione-S-transferase expression vector pGEX-4T, the cDNA fragment could be expressed into a fusion **protein** that

specifically reacted with MAb 3H11. Moreover, the fusion **protein** could competitively inhibit MAb 3H11 binding to MGC 803 cells. Based on the **nucleotide** sequence of the cDNA fragment, the full length of the cDNA (2156 bp) was obtained by Rapid-Amplification-cDNA-End (RACE) and **nested PCR**. Its reading frame was 1767 bp encoding a **protein** of 589 amino acids. Sequence analysis indicated that there is no highly homologous gene in the GenBank. Northern blot and RT-PCR showed that the mRNA of MAb 3H11 antigen was extensively distributed in embryonic tissue and in different cancerous tissues, but not in corresponding normal tissues. Moreover, in producing **antibodies** to the antigen expressed prokaryotically, we found that the immunogenicity of the antigen was low in mammalian. Thus we believe that this novel antigen acts as an expression regulator in embryo cells and regains expression in tumor cells. In addition, this antigen is characterized by low differentiation and high proliferation. Molecular function of the antigen needs to be investigated.

L144 ANSWER 24 OF 45 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2

ACCESSION NUMBER: 2001:197602 BIOSIS
DOCUMENT NUMBER: PREV200100197602
TITLE: Keratin 9 is a component of the perinuclear ring of the manchette of rat spermatids.
AUTHOR(S): Mochida, Kazuhiko; Rivkin, Eugene; Gil, Mara; Kierszenbaum, Abraham L. (1)
CORPORATE SOURCE: (1) Department of Cell Biology and Anatomical Sciences, CUNY Medical School, 138th Street and Convent Avenue, J-903, New York, NY, 10031: kier@med.cuny.edu USA
SOURCE: Developmental Biology, (November, 2000) Vol. 227, No. 2, pp. 510-519. print.
ISSN: 0012-1606.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Previous work in our laboratory has shown that a 62- to 64-kDa **protein** was a major component of the perinuclear ring of manchettes fractionated from rat spermatids. Mass spectrometry analysis of this **protein** indicated the presence of a glycine-rich domain homologous to human keratin 9 (K9). Several **antibodies** to K9, raised against synthetic peptides of human K9, recognized the 64- to 62-kDa **protein** in the perinuclear ring of the manchette as well as in keratinocytes of the suprabasal layer of the rat and human footpad/sole epidermis in both immunoblotting and immunocytochemical experiments. Based on these data, human-derived K9 primers were used to clone rat K9 cDNA from epidermis by RT-PCR. Rat-specific K9 primers were then used to perform a two-step (**nested**) **PCR** to amplify the K9-specific rat testicular RNA and to obtain cDNA to demonstrate K9 gene expression in rat testis. The deduced amino acid sequence of rat K9 cDNA contains 618 amino acids with an estimated molecular mass of 63,020 Da, in agreement with that obtained by electrophoretic fractionation of rat manchette and epidermis footpad **proteins**. The deduced **protein** structure correlates with the recognizable pattern of keratins: a rod domain of 304 amino acids with well-conserved initiation and termination sequences (MQNLNSRLASY and EIETYRKLLEG, respectively), flanked by glycine/serine-rich head and tail domains of 141 and 173 amino acids, respectively. A high content of phenylatanine was detected in the head domain and a repetitive motif (SGGSYGGGS) in the tail domain. A comparison with human keratin 9 showed an overall **nucleotide** and amino acid similarity of 75%. An increased level of K9 transcripts was detected in a cDNA **library** prepared from fractionated round spermatids. Results of this study show that rat testis expresses K9 and that this **protein** is a component the perinuclear ring of the manchette of rat spermatids.

L144 ANSWER 25 OF 45 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:245097 BIOSIS
DOCUMENT NUMBER: PREV200100245097
TITLE: Identification of a novel human polyamine acetyltransferase.
AUTHOR(S): Coleman, Catherine S. (1); Chau, Vincent (1); Pegg, Anthony E. (1)
CORPORATE SOURCE: (1) Pennsylvania State University College of Medicine, 500 University Drive, Hershey, PA, 17033 USA
SOURCE: FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A169. print.
Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology 2001 Orlando, Florida, USA March 31-April 04, 2001
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The polyamines spermidine, spermine and their diamine precursor putrescine are essential for growth and differentiation of mammalian cells. Polyamine content in mammalian cells is tightly controlled at the levels of both synthesis and degradation. The rate-limiting factor in degradation is acetylation of spermidine and spermine, which leads to either further metabolism or excretion. This process is thought to be initiated by the enzyme spermidine/spermine-N1-acetyltransferase (SSAT-1), which is highly inducible by polyamines, polyamine analogs and other stimuli. We have now identified a second human SSAT, hereafter referred to as SSAT-2. The encoded amino acid sequence of human SSAT-2 shares 45% identity and 66% homology with human SSAT-1 but is only distally related to other known members of the N-acetyltransferase family. The tissue distribution of SSAT-1 and SSAT-2 was compared by using RT-PCR to screen for the presence of transcripts in multiple tissue panels (Clontech). mRNA for SSAT-1 and SSAT-2 was present in all tissues tested and showed similar levels of expression when normalized. The SSAT-2 gene was cloned from a HeLa cell **library** by **nested PCR**, expressed in E.coli from a pT7 expression plasmid and purified as a 6XHistidine **tagged protein**. Preliminary results indicate that SSAT-2 acetylates putrescine, spermidine and spermine with Km values in the low mM range. Interestingly, while N1-acetylspermidine is the predominant product formed using spermidine as a substrate for assay. SSAT-2 also forms significant amounts of N8-acetylspermidine. This is in contrast to SSAT-1 which acetylates spermidine exclusively at the N1-position. Although the physiological significance of SSAT-2 in normal and diseased states remains to be determined, it is interesting that organisms such as C.elegans and S. pombe have only a single SSAT-like gene that is closer in sequence to SSAT-2 than SSAT-1.

L144 ANSWER 26 OF 45 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1998:490753 BIOSIS
DOCUMENT NUMBER: PREV199800490753
TITLE: In vitro method for the generation of **protein libraries** using PCR amplification of a single DNA molecule and coupled transcription/translation.
AUTHOR(S): Ohuchi, Shoji; Nakano, Hideo (1); Yamane, Tsuneo
CORPORATE SOURCE: (1) Lab. Molecular Biotechnol., Dep. Biological Mechanisms Functions, Graduate Sch. Biological Agricultural Sci., Nagoya Univ., Furo-cho, Chikusa-ku, Nagoya 464-8601 Japan
SOURCE: Nucleic Acids Research, (Oct. 1, 1998) Vol. 26, No. 19, pp. 4339-4346.
ISSN: 0305-1048.
DOCUMENT TYPE: Article
LANGUAGE: English

AB A novel in vitro method for the generation of a **protein library** has been developed using the polymerase chain reaction (PCR) amplification of a single DNA molecule followed by in vitro coupled transcription/translation. DNA template encoding green fluorescent **protein** of a jellyfish Aequorea victoria was extensively diluted to one molecule per well, and then amplified by a total of 80 cycles of **PCR** with **nested** primers. The exact number of origins in the amplified DNA fragment was then estimated by directly sequencing a part of the fragment, at which an individual template molecule was marked by PCR with a primer containing three randomized bases. Since the sequences obtained in 91 independent amplifications were diversified statistically, each amplified fragment was likely originated from a single DNA molecule. In addition, the amplified fragments served as a template for in vitro coupled transcription/translation using T7 RNA polymerase and Escherichia coli S30 extract. These results suggest that the **library** obtained by the PCR amplification of a single DNA molecule diluted from a variety of DNA pools is potentially useful in **high -throughput** generation of **protein libraries**.

L144 ANSWER 27 OF 45 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 2002:34461420 BIOTECHNO
TITLE: Identification of a novel mutation in the arginine vasopressin-neurophysin II gene in familial central diabetes insipidus
AUTHOR: Bullmann C.; Kotzka J.; Grimm T.; Heppner C.; Jockenhovel F.; Krone W.; Muller-Wieland D.
CORPORATE SOURCE: Dr. D. Muller-Wieland, Deutsches Diabetes-Forschungsinst., D-40225 Dusseldorf, Germany. E-mail: mueller-wieland@ddfi.uni-duesseldorf.de
SOURCE: Experimental and Clinical Endocrinology and Diabetes, (2002), 110/3 (134-137), 20 reference(s) CODEN: ECEDFQ ISSN: 0947-7349
DOCUMENT TYPE: Journal; Article
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Familial central diabetes insipidus is an inherited disease of predominant autosomal dominant trait characterized by a deficiency of arginine vasopressin. The arginine vasopressin-neurophysin II (AVP-NPII) gene consists of three exons and is located on chromosome 20p13 encoding for the precursor **protein** of AVP. We investigated two Caucasian families with a typical autosomal dominant trait of familial central diabetes insipidus, defined by deficiency of arginine vasopressin. After **PCR** amplification of exon 1 and exon 2/3, fragments were pooled and purified. **Nucleotide** sequencing was performed with the Taq DyeDeoxy-terminator cycle sequencing method using **nested** primers. Two mutations in the coding region of NPII were identified. In family C we found a heterozygous G .rtwarw. C missense mutation (AA61) in exon 2 leading to the substitution of cystein with serine. In family D a novel heterozygous nonsense mutation in exon 3 (AA 83, GAG .rtwarw. **TAG**) was indentified, leading to a stop codon instead of glutamine. Both mutations were confirmed by restriction analysis and were found in all affected but not in healthy family members or control subjects. We therefore have identified a missense mutation of the AVP-NPII gene and a novel mutation predicting a truncated **protein**
.

L144 ANSWER 28 OF 45 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 2001:32951810 BIOTECHNO
TITLE: Development of a yeast stop codon assay readily and generally applicable to human genes
AUTHOR: Kataoka A.; Tada M.; Yano M.; Furuuchi K.; Cornain S.; Hamada J.-I.; Suzuki G.; Yamada H.; Todo S.; Moriuchi

T.
CORPORATE SOURCE: Dr. M. Tada, Division of Cancer-Related Genes, Institute for Genetic Medicine, Hokkaido University, N-15 W-7, Kitaku, Sapporo 060-0815, Japan. E-mail: m_tada@med.hokudai.ac.jp
SOURCE: American Journal of Pathology, (2001), 159/4 (1239-1245), 18 reference(s) CODEN: AJPAA4 ISSN: 0002-9440
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We established a yeast-based method to screen chain-terminating mutations that is readily applicable to any gene of interest. Based on the finding that 18- to 24-base-long homologous sequences are sufficient for gap repair in vivo in yeast, we used a strategy to amplify a test-gene fragment with addition of 24-bp sequences homologous to both cut-ends of a yeast expression vector, pMT18. After co-transformation with the amplified fragment and the linearized pMT18, each yeast (Saccharomyces cerevisiae) cell automatically forms a single-copy circular plasmid (because of CEN/ARS), which expresses a test-gene::ADE2 chimera **protein**. When the reading frame of the test-gene contains a nonsense or frameshift mutation, truncation of the chimera **protein** results in lack of ADE2 activity, leading to formation of a red colony. By using a **nested polymerase chain** reaction using proofreading Pfu polymerase to ensure specificity of the product, the assay achieved a low background (false positivity). We applied the assay to BRCA1, APC, hMSH6, and E-cadherin genes, and successfully detected mutations in mRNA and genomic DNA. Because this method - universal stop codon assay - requires only 4 to 5 days to screen a number of samples for any target gene, it may serve as a **high-throughput** screening system of general utility for chain-terminating mutations that are most prevalent in human genetic diseases.

L144 ANSWER 29 OF 45 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 2000:30320866 BIOTECHNO
TITLE: Development of an immunoenzymatic assay for the detection of human antibodies against Trypanosoma cruzi calreticulin, an immunodominant antigen
AUTHOR: Marcelain K.; Colombo A.; Molina M.C.; Ferreira L.; Lorca M.; Aguillon J.C.; Ferreira A.
CORPORATE SOURCE: A. Ferreira, Instituto de Ciencias Biomedicas, Facultad de Medicina, Universidad de Chile, Casilla 13898, Correo 21, Santiago, Chile. E-mail: aferreir@machi.med.uchile.cl
SOURCE: Acta Tropica, (31 MAY 2000), 75/3 (291-300), 18 reference(s) CODEN: ACTRAQ ISSN: 0001-706X
PUBLISHER ITEM IDENT.: S0001706X00000620
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We have developed an indirect immunoenzymatic assay (ELISA) for the detection of human antibodies against calreticulin (formerly known as Tc45), a dimorphic Trypanosoma cruzi antigen, described in our laboratory. PVC microtitration plates were sensitized with the monoclonal anti-calreticulin antibody (MoAb) and reacted with calreticulin present in a partially purified preparation. The presence of anti-T. cruzi calreticulin IgG in sera from infected individuals was tested. The data generated with this assay were validated by correlation, in a regression analysis, with those obtained by an indirect immunoradiometric assay

(IRMA). From the 12 seropositive sera (as defined by a commercial test), eight came out positive and four negative in both assays. The 12 human sera were also analyzed in direct immunometric assays (ELISA and IRMA), where the solid phase was sensitized with a whole parasite extract. The direct ELISA and IRMA correlated positively ($P < 0.01$). Further validation of this ELISA was achieved with an indirect immunofluorescense assay. The high degree of significance obtained when the indirect IRMA and ELISA systems were compared, indicated that the relatively small sample number used (12) was statistically satisfactory for the purposes of this investigation. Thus, the IRMA can be replaced by the ELISA, with advantages mainly derived from the cumbersome manipulation of radioactive wastes. The MoAb used as an antigen **capture agent** in the ELISA proposed here, recognizes a homologous **protein** in Trypanosoma rangeli, suggesting that individuals infected with this parasite might have crossreactive antibodies. However, the system retains its diagnostic interest, given the facts that the MoAb does not recognize a homologous **protein** in Leishmania mexicana, Leishmania donovani, or Crithidia fasciculata. (C) 2000 Elsevier Science B.V.

L144 ANSWER 30 OF 45 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 1999:30035646 BIOTECHNO
TITLE: CTp11, a novel member of the family of human cancer/testis antigens
AUTHOR: Zendman A.J.W.; Cornelissen I.M.H.A.; Weidle U.H.; Ruiter D.J.; Van Muijen G.N.P.
CORPORATE SOURCE: A.J.W. Zendman, Department of Pathology, University Hospital, P. O. Box 9101, 6500 HB Nijmegen, Netherlands.
E-mail: H.Zendman@pathol.azn.nl
SOURCE: Cancer Research, (15 DEC 1999), 59/24 (6223-6229), 41 reference(s)
CODEN: CNREA8 ISSN: 0008-5472
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AB To identify new genes that may contribute to the metastatic pathway of neoplastic cells, we compared mRNA expression of the parental human melanoma cell line 1F6 and its metastatic variant 1F6m using mRNA differential display. We isolated a cDNA clone that was exclusively expressed in 1F6m. Northern blot analysis on a broader panel of human melanoma cell lines with different metastatic capacity following s.c. inoculation into nude mice demonstrated that the gene was expressed only in the most aggressive, highly metastatic cell lines, giving a band of 0.5 kb. The isolated full length cDNA clone showed an open reading frame of 97 amino acids. To study the subcellular localization of the gene product, COS-1 cells were transfected with cDNA of the gene fused to eGFP. We found the fusion **protein** to be exclusively present in the nucleus. A computer search showed strong homology with human genomic clones all localized on chromosome X (Xq26.3-Xq27.1) and with several expressed sequence **tags**, all from testis. Localization of the gene on chromosome X was confirmed by genomic **PCR** on a panel of human chromosome-specific rodent/human hybrid cell lines. Northern blotting and reverse transcription-**PCR** on 17 different normal human tissue samples showed that the gene was only expressed in normal testis. Reverse transcription-**PCR** on a great number of different human tumor cell lines showed expression in 25-30% of the melanoma and bladder carcinoma cell lines. Only 2 of 29 other tumor cell lines were positive. **Nested PCR** analysis of a series of fresh human melanocytic tumors demonstrated expression in 7 of 10 melanomas tested. No expression was seen in benign melanocytic tumors. In addition to melanoma, some malignant tumors from other histological types were also found to be positive. Based on these data, we conclude that the

described gene, CTp11 (cancer/testis-associated **protein** of 11 kDa), is a novel member of the family of cancer/testis antigens.

L144 ANSWER 31 OF 45 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 1999:29585411 BIOTECHNO
TITLE: Tissue distribution of a novel cell binding **protein**, osteoadherin, in the rat
AUTHOR: Shen Z.; Gantcheva S.; Sommarin Y.; Heinegard D.
CORPORATE SOURCE: D. Heinegard, Section Connective Tissue Biology, Dept. Cell and Molecular Biology, University of Lund, Lund, Sweden.
E-mail: dick.heinegard@medkem.lu.se
SOURCE: Matrix Biology, (1999), 18/6 (533-542), 23 reference(s)
CODEN: MTBOEC ISSN: 0945-053X
PUBLISHER ITEM IDENT.: S0945053X99000487
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Osteoadherin is a cell binding keratan sulfate proteoglycan which was recently isolated from mineralized bovine bone and subsequently cloned and sequenced. For studies of osteoadherin expression in rat tissues we isolated and sequenced a 1.3-kbp partial cDNA covering most of the coding region using a rat calvaria cDNA **library**. The most 5' end of the cDNA was obtained by reverse transcription **PCR** from the bone total RNA preparation. The deduced, translated **protein** sequence containing 423 amino acid residues shows high sequence identity to mouse, bovine and human osteoadherin except in the very acidic C-terminal region. However, the rat counterpart showed a similarly high content of acidic amino acid residues. Ribonuclease protection assay showed osteoadherin mRNA to be expressed in femoral bone and calvaria tissues, while no expression was detected in cartilage, tendon or liver. Using very sensitive **nested** RT-**PCR**, however, message was detected in femoral head, rib, tendon and bone marrow total RNA preparations. An antiserum specific for the rat C-terminal region of osteoadherin was generated and used for studies of **protein** distribution by immunohistochemistry during femoral head development. Osteoadherin was primarily present in bone trabeculae and no staining was seen in cartilage. In situ hybridization showed the strongest expression in osteoblasts close to the cartilage/bone interface of the growth plate and lower expression in diaphyseal osteoblasts. On maturation of the femoral head on day 60 some expression was detected immediately below the forming articular cartilage. Our data indicated that osteoadherin is primarily expressed by osteoblasts and might have a role in regulation of mineralization. Copyright (C) 1999 Elsevier Science B.V./International Society of Matrix Biology.

L144 ANSWER 32 OF 45 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 1997:27368310 BIOTECHNO
TITLE: Hepatitis B virus mutants in hepatocellular carcinoma patients with coexisting HBsAg and anti-HBs.sup.1
AUTHOR: Young Nyun Park; Nakai K.; Park C.; Abe K.
CORPORATE SOURCE: K. Abe, Department of Pathology, Natl. Inst. of Infectious Diseases, Toyama 1-23-1, Shinjuku-ku, Tokyo 162, Japan.
E-mail: kenjiabe@nih.go.jp
SOURCE: Hepatology Research, (1997), 8/1 (52-62), 30 reference(s)
CODEN: HPRSFM ISSN: 0928-4346
PUBLISHER ITEM IDENT.: S138663469700051X
DOCUMENT TYPE: Journal; Article
COUNTRY: Ireland

LANGUAGE: English
SUMMARY LANGUAGE: English
AB We analyzed the sequence of S, precore, and X genes of the hepatitis B virus (HBV) genome in four Korean hepatocellular carcinoma (HCC) patients who were seropositive for both HBsAg and anti-HBs. HBV DNA was extracted from formalin-fixed, paraffin-embedded liver tissues, and then amplified by **nested PCR** and sequenced. We found a point mutation in the S gene of 2 cases, resulting in conversion from IIe-126 or Thr-126 of the wild type virus to Ser-126. Three of four patients had a precore sequence with a frame **TAG** stop codon. Interestingly, all patients revealed **nucleotide** changes in enhancer II region of the X gene, especially the binding region of the nuclear factor CCAAT/enhancer binding **protein**. Three showed a point mutation of T to C at **nucleotide** position 1753 and one patient showed a 19-base pair deletion resulting in a frame shift with three novel amino acids followed by the stop codon. No mutation was observed in the HBV genomes isolated from HCC patients with HBsAg alone. Although our data are preliminary, these results suggest that mutations of the X gene and common antigenic domain within 'a' loop of the S gene may be related to the phenomenon in unusual serological findings such as coexistence of HBsAg and anti-HBs.

L144 ANSWER 33 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2002-547524 [58] WPIDS
DOC. NO. CPI: C2002-155215
TITLE: Determining biological effect of compound on gene expression of cell, comprises obtaining nuclear extract from cells exposed to compound and combining it with nucleic acid containing cis-binding site for forming the complexes.
DERWENT CLASS: B04 D16
INVENTOR(S): ADAMS, C C; HARPER, M E; LABHART, P
PATENT ASSIGNEE(S): (CIST-N) CISTEM MOLECULAR CORP
COUNTRY COUNT: 97
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002038734	A2	20020516	(200258)*	EN	43

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2002032510 A 20020521 (200260)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002038734	A2	WO 2001-US46927	20011109
AU 2002032510	A	AU 2002-32510	20011109

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002032510	A Based on	WO 200238734

PRIORITY APPLN. INFO: US 2000-248339P 20001113
AB WO 200238734 A UPAB: 20020910
NOVELTY - Determining (M1) biological effect of compound on transcription

factor binding activity profile of cell comprising obtaining nuclear extract (NE) from cells exposed to compound, combining NE with nucleic acid (NA) containing cis-binding site under conditions that allow formation of transcription factor/cis site (TFCS) complexes, and comparing TFCS complex formed with the control TFCS complexes, is new.

DETAILED DESCRIPTION - Determining (M1) biological effect of compound on transcription factor binding activity profile of cell comprising obtaining NE from cells exposed to the compound, combining NE with NA containing a cis-binding site under conditions that allow formation of TFCS complexes, and comparing if any TFCS complex formed as a result differs from TFCS complexes formed by combining NA with a control NE obtained from cells not exposed to the compound, is new.

USE - M1 is useful for determining a biological effect of a compound on a transcription factor binding activity profile of a cell, where the cell is selected from vertebrate cell, diseased cell, normal cell, or a pathogen. The cell is mammalian cell selected from canine, equine, feline, murine, ovine, porcine, and primate cells, a human cell, a diseased cell selected from cancer cell, infected cell, abnormal T cell, or abnormal neuronal cell, or a pathogen selected from eukaryotic cell, prokaryotic cell or a virus (claimed).

Dwg.0/2

L144 ANSWER 34 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2002-463310 [49] WPIDS
DOC. NO. CPI: C2002-131718
TITLE: **High-throughput** screening for internalizing antibodies and identifying ligands that are internalized into a cell, comprises detecting the presence of a reporter within the cell that has been contacted with a ligand.
DERWENT CLASS: B04 D16
INVENTOR(S): KIRPOTIN, D B; MARKS, J D; NIELSEN, U B
PATENT ASSIGNEE(S): (REGC) UNIV CALIFORNIA
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002033044	A2	20020425	(200249)*	EN	71

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

AU 2002013286 A 20020429 (200255)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002033044	A2	WO 2001-US32311	20011017
AU 2002013286	A	AU 2002-13286	20011017

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002013286	A	Based on	WO 200233044

PRIORITY APPLN. INFO: US 2000-241279P 20001018
AB WO 200233044 A UPAB: 20020802
NOVELTY - Identifying ligands that are internalized into a cell comprising

detecting the presence of a reporter within the cell that has been contacted with a ligand, where the presence of the reporter within the cell indicates that the ligand is internalized into the cell, is new.

DETAILED DESCRIPTION - Identifying ligands that are internalized into a cell comprising:

(a) contacting the cell with a reporter non-covalently coupled to a ligand;

(b) dissociating the reporter from the ligand and removing dissociated reporter from the surface of the cell; and

(c) detecting the presence of the reporter within the cell, where the presence of the reporter within the cell indicates that the ligand is internalized into the cell, is new.

INDEPENDENT CLAIMS are also included for the following:

(1) screening a cell for a receptor that internalizes a ligand;

(2) a ligand library comprising a several members that comprise ligands and epitope tags, where the ligands vary between members of the library and the epitope tags are constant;

(3) a construct for screening a cell for an internalizing receptor, where the construct comprises a ligand non-covalently coupled to an effector through an epitope tag;

(4) a kit for identifying an internalizing cell or for screening a ligand that is internalized by a cell, comprising a container with the ligand library cited above;

(5) identifying internalizing receptors;

(6) screening an agent for the ability to modulate internalization of a ligand into a cell;

(7) a metal chelating lipid comprising a lipid, a hydrophilic polymer and a metal chelation group attached to the hydrophilic polymer;

(8) delivering an effector to a cell; and

(9) a composition comprising:

(a) a lipid, a hydrophilic polymer, and a chelation group attached to the hydrophilic polymer and capable of forming a chelation bond with an epitope tag;

(b) a ligand comprising the epitope tag, where the ligand binds and is optionally internalized by a cell; and

(c) an effector associated with the lipid.

USE - The method is useful for **high-throughput** screening for internalizing antibodies and identifying ligands that are internalized into a cell. The method allows the study of receptors function and the determination of the temporal-spatial pattern of receptor expression. The cell-specific receptor ligand, more preferably internalizing cell specific receptor ligand is useful for targeting drugs or markers to the cell surface or into the cytoplasm (for internalizing receptors) e.g. for therapeutic effect.

Dwg.0/8

L144 ANSWER 35 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2002-471270 [50] WPIDS
DOC. NO. NON-CPI: N2002-372055
DOC. NO. CPI: C2002-133956
TITLE: Producing **proteins** having full-length, correctly folded domains and marker moiety-**tagged** N- or C-terminals, by genetically modifying cDNA to encode individual **protein** having marker moiety fused to N- or C-terminus.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BLACKBURN, J M; KOZLOWSKI, R; MULDER, M A; SAMADDAR, M
PATENT ASSIGNEE(S): (SENS-N) SENSE PROTEOMIC LTD
COUNTRY COUNT: 97
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2002027327 A2 20020404 (200250)* EN 47
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO
RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2001079948 A 20020408 (200252)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002027327 A2		WO 2001-GB3693	20010817
AU 2001079948 A		AU 2001-79948	20010817

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001079948 A		Based on	WO 200227327

PRIORITY APPLN. INFO: US 2000-247995P 20001114; GB 2000-20357 20000817

AB WO 200227327 A UPAB: 20020807
NOVELTY - Producing full-length **proteins** incorporating alpha -S-dNTPs and dNTPs into DNA (I) encoding **protein** (P), protecting ends of (I) from nuclease digestion, generating (I) in which set of **nested** deletions are generated and 5' or 3' untranslated region (UTR) of open reading frame (ORF) are removed, by nuclease digestion, cloning fragments into vector having coding sequence for 5'/3' marker moiety, and expressing **proteins**, is new.

DETAILED DESCRIPTION - Producing (M1) one or more **proteins** (P) in which one or more domains are full length and correctly folded and which are each **tagged** at either N- or C-terminus with one or more marker moieties (MM), comprising:

(a) amplifying DNA molecules (I) having open reading frame (ORF) encoding (P) together with 5' and/or 3' untranslated regions (UTR) under conditions that statistically incorporate alpha -S-dNTPs as well as dNTPs into daughter (I);

(b) specifically protecting 5' and 3' end of (I) from nuclease digestion; treating (I) first with a 5' to 3' or 3' to 5'-nuclease to generate a set of **nested** deletions followed by treating with a single-strand nuclease under conditions that allow removal of the 5' or 3' UTR including start or stop codons of ORF;

(c) cloning generated fragments into expression vector containing a coding sequence for one or more 5' or 3' MM; and

(d) expressing encoded (P).

INDEPENDENT CLAIMS are also included for the following:

(1) a **library** of **tagged proteins** (II) produced by (M1);

(2) producing (M2) a **protein** array, comprising:

(a) clonally separating each member of (II);

(b) expressing the individual **tagged proteins** in a spatially separated format;

(c) purifying each **tagged protein** by marker moiety; and

(d) depositing each **protein** into a spatially defined array; and

(3) an array (III) comprising **proteins** prepared by (M1), or produced by (M2);

(4) screening a **protein** function or abundance, comprising contacting **antibody** array generated using (II), with a mixture

of one or more **proteins**.

USE - (III) is useful for screening one or more compounds for biological activity which involves contacting one or more compounds with (III) and measuring binding of the one or more compounds to the **proteins** in the array. (III) is useful for screening one or more **proteins** for specific **protein-protein** interactions or **protein-nucleic acid** interactions which involves contacting one or more **proteins** e.g. a cell surface receptor, or contacting one or more **nucleic acid** probes with (III), and measuring binding of one or more specific **proteins** or measuring binding of probes to the **proteins** in the array, respectively. (III) is useful in the rapid screening of a **protein**, compound or **nucleic acid**, and also for screening for molecules (preferably, **antibodies**) which recognize each **protein** in the array. (III) is also useful for generating an **antibody** array which involves contacting (III) with an **antibody library** such that one or more **proteins** in the **protein** array bind to at least one **antibody** in the **antibody library**, removing any unbound **antibodies** and immobilization of those **antibodies** bound to **proteins** in the **protein** array. The methods as described above also comprise providing (III), where the **proteins** in (III) are purified and immobilized in a single step. The **tagged proteins** produced by (M1) are useful for analysis of interaction between expressed **protein** and other **proteins**, immobilization on an affinity column/substrate for example to allow the purification by affinity chromatography of, interacting **proteins**, DNA or chemical compounds; in the immobilization by affinity purification for interrogation by **antibodies** as a diagnostic tool, as a probe for cDNA microarray for identifying DNA binding **proteins**; or for elucidating the identity of **proteins** in the proteome, where mass spectrometric analysis of expressed **protein** components of source **library** or start material modified by the methods, are performed. The **antibody** arrays produced using (I) are useful for screening of **protein** function or abundance. (All claimed).

ADVANTAGE - The method allows the **tag** to be inserted in the correct reading frame either precisely at the N- or C-terminus of each **protein**, or within a region close to either terminus which is unimportant in the folding and function of the **protein**, so that the individual **tagged proteins** fold correctly and hence retain function when specifically immobilized in the array. In the case of multidomain **proteins** where individual domains have discrete functions, the method also allows insertion of the **tag** within the overall coding sequence but outside specific domain boundaries so that the individual **tagged** domains fold correctly and hence retain function when specifically immobilized in the array. The methods allow the specific modification, in one pot, of every member of a cDNA **library** in a manner which does not rely on any knowledge of the sequence of the individual genes. Instead, it relies on non-processive truncation of each cDNA by a nuclease so that either the 5'- or the 3'-untranslated region of each cDNA is removed.

Dwg.0/1

L144 ANSWER 36 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-611112 [70] WPIDS
DOC. NO. NON-CPI: N2001-456193
DOC. NO. CPI: C2001-182476
TITLE: Identifying and/or characterizing peptide, comprises analyzing peptide map containing peptide and its primary structure fingerprint by mass spectrometry, and comparing obtained data with reference database.

DERWENT CLASS: B04 D16 S03 V05
INVENTOR(S): CAHILL, D J; EICKHOFF, H; KLOSE, J; LEHRACH, H; NORDHOFF, E; SCHMIDT, F
PATENT ASSIGNEE(S): (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001057519	A2	20010809	(200170)*	EN	55

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001035456 A 20010814 (200173)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001057519	A2	WO 2001-EP1332	20010207
AU 2001035456	A	AU 2001-35456	20010207

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001035456	A	Based on	WO 200157519

PRIORITY APPLN. INFO: EP 2000-102567 20000207

AB WO 200157519 A UPAB: 20011129
NOVELTY - Identifying (M1) and/or characterizing a (poly)peptide (I), comprising:

(a) analyzing a peptide map of (I) containing at least 1 peptide and its primary structure fingerprint by mass spectrometry (MS); and

(b) comparing the obtained data with a reference database containing MS data of peptide maps, containing at least 1 peptide and its primary structure fingerprint of one or a variety of (poly)peptides, is new.

USE - The method is useful for identification and/or characterization of a (poly)peptide (claimed). The method is useful for applications where it is desired or needed to have direct access to the genetic information encoding the polypeptide the minimal protein identifiers (MPI) of which has been found in the database. The method is also useful for the development of pharmaceuticals and/or diagnostics.

ADVANTAGE - The method allows for the identification and/or characterization of proteins in a large scale, short time and in **high throughput** under low costs. Identification and characterization of polypeptide is carried out without knowing its amino acid sequence and/or other structural features. The method allows simultaneous identification and/or characterization of a large number of different polypeptide due to the high resolution of the employed two-dimensional electrophoresis, but also the assignment of functional parameters to the analyzed polypeptide. The method also allows for the generation of MPIs interalia taking into account of a polypeptide that may not occur e.g., when a eukaryotic polypeptide is recombinantly produced in a prokaryotic host.

Dwg.0/10

L144 ANSWER 37 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-496932 [54] WPIDS
CROSS REFERENCE: 2001-442253 [47]; 2001-442255 [47]; 2001-451890 [48];

2001-451908 [48]; 2001-451909 [48]; 2001-451912 [48];
2001-451938 [48]; 2001-451939 [48]; 2001-457603 [49];
2001-457740 [49]; 2001-465363 [50]; 2001-465571 [50];
2001-465578 [50]; 2001-465705 [50]; 2001-476114 [51];
2001-476164 [51]; 2001-476197 [51]; 2001-476198 [51];
2001-476199 [51]; 2001-476282 [51]; 2001-476283 [51];
2001-483140 [52]; 2001-483233 [52]; 2001-488707 [53];
2001-488788 [53]; 2001-488875 [53]; 2001-488895 [53];
2001-496929 [54]; 2001-496930 [54]; 2001-496931 [54];
2001-514838 [56]; 2001-522358 [57]; 2001-565565 [63];
2001-582152 [65]; 2001-582153 [65]; 2001-589862 [66];
2001-589934 [66]; 2001-607699 [69]; 2001-611724 [70];
2001-611725 [70]; 2001-626375 [72]; 2001-626426 [72];
2001-626432 [72]; 2001-626527 [72]; 2001-639362 [73];
2002-010428 [01]; 2002-025688 [03]; 2002-062370 [08];
2002-280918 [32]; 2002-575369 [61]; 2002-590824 [63];
2002-674924 [72]

DOC. NO. CPI: C2001-149290

TITLE: Novel human secreted CUB domain polypeptide for treating bone fracture, to assist in the treatment of cartilage repair and healing, to control osteonecrosis, bone and cartilage tumor growth and collagen formulation.

DERWENT CLASS: B04 D16

INVENTOR(S): ARTERBURN, M C; BOYLE, B J; DRMANAC, R T; LIN, H; LIU, C; MIZE, N K; TANG, Y T

PATENT ASSIGNEE(S): (HYSE-N) HYSEQ INC

COUNTRY COUNT: 94

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001057267	A1	20010809	(200154)*	EN	129

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001036721 A 20010814 (200173)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001057267	A1	WO 2001-US3905	20010205
AU 2001036721	A	AU 2001-36721	20010205

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001036721	A Based on	WO 200157267

PRIORITY APPLN. INFO: US 2000-678216 20000929; US 2000-496914 20000203; US 2000-560875 20000427

AB WO 200157267 A UPAB: 20021113

NOVELTY - An isolated CUB domain polypeptide (I) comprising a sequence having at least 80% identity to a sequence (S1) comprising 110, 15, 95 or 61 amino acids fully defined in the specification, its translated protein coding portion, mature protein coding portion, extracellular portion or active domain, or a polypeptide with CUB domain activity comprising at least ten consecutive amino acids of S1, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the

following:

(1) an isolated polynucleotide (II) comprising a sequence (S2) of 402, 754 or 333 nucleotides fully defined in the specification, its translated protein coding portion, mature protein coding portion, extracellular portion, or active domain;

(2) an isolated polynucleotide encoding a polypeptide with biological activity, which hybridizes to the complement of (II);

(3) an isolated polynucleotide encoding a polypeptide with biological activity, having greater than 90% sequence identity with (II);

(4) an isolated polynucleotide comprising the complement of (II);

(5) a vector (III) comprising (II);

(6) an expression vector (IV) comprising (II);

(7) a host cell (V) genetically engineered to express (II);

(8) a composition (C) comprising (I);

(9) a polynucleotide encoding (I);

(10) an antibody (Ab) specific for (I);

(11) detecting (II) in a sample, by:

(a) contacting the sample with a compound that forms a complex with (II) and detecting the complex, so that if a complex is detected, (II) is detected; or

(b) contacting the sample with nucleic acid primers that anneal to (II), amplifying a product comprising at least a portion of (II), and detecting the product, thereby detecting (II) in the sample;

(12) detecting (I) in a sample, by contacting the sample with a compound that binds to and forms a complex with (I), and detecting formation of the complex, so that if a complex formation is detected, (I) is detected;

(13) identifying a compound that binds to (I), by:

(a) contacting the compound with (I) and for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if polypeptide/compound complex is detected, a compound that binds to (I) is identified;

(b) contacting the compound with (I), in a cell, for a time sufficient to form a polypeptide/compound complex, where the complex drives expression of a reporter gene sequence in the cell; and

(c) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to (I) is identified;

(14) producing (I);

(15) a kit comprising (I);

(16) a nucleic acid array (VI) comprising (II) or a unique segment of (II) attached to a surface;

(17) treating a subject in need of enhanced activity or expression of (I), by administering (I), (II) or agonist of (I); and

(18) treating a subject in need to inhibit the activity or expression of (I), by administering a polypeptide that competes with (I), a polynucleotide that inhibits the expression of (II), or antagonist of (I).

ACTIVITY - Cytostatic; neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiinflammatory; dermatological; immunosuppressive; antianemic; neuroprotective; nootropic; vulnerary; antiparkinsonian; anticonvulsant; cerebroprotective; antiHIV; virucide; antibacterial; fungicide; immunostimulant; vasotropic; antidiabetic.

MECHANISM OF ACTION - Gene therapy.

No supporting data given.

USE - (VI) detects full-matches or mismatches to the polynucleotide or a unique segment of (II) (claimed).

(I) and (II) are useful for treating and/or preventing bone fracture and bone growth, to assist in the treatment of cartilage repair and healing, to control osteonecrosis, to control bone and cartilage tumor growth, to modulate collagen formulation and to modulate growth and development of other tissues and organs. (I) and (II) are also useful during artificial insemination and in vitro fertilization to protect the sperm head and provide guidance cues.

(I) and (II) are also useful as nutritional sources or supplements, and for treating nervous system disorders including traumatic, ischemic, neurological, infectious, demyelinated, or degenerative lesions, lesions associated with nutritional diseases or disorders or lesions caused by toxic substances. (I) is also useful in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers. (C) is useful for proliferation of neural cells and nerve regeneration, for treating peripheral nervous system diseases, central nervous system diseases, e.g., Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome, mechanical and traumatic disorders, e.g., spinal cord disorders, head trauma and cerebrovascular diseases such as stroke, peripheral neuropathies resulting from chemotherapy or other medical therapies.

(I) is useful in the treating of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), caused by genetic alterations, by viral (e.g., HIV), bacterial or fungal infections or by autoimmune disorders, e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes and modulating cytolytic activity of NK cells and other cell populations. (I) is useful for treating coagulation disorders (including hereditary disorders, such as hemophilias), to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes, and for treating cancer.

(C) is also useful to promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, in the generation or regeneration of other tissues, for promoting the growth of cells comprising such tissues, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage, for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells, and for inhibiting the growth of tissues. (C) is useful for dissolving or inhibiting formation of thromboses, and for treatment and prevention of resulting conditions.

Dwg.0/3

L144 ANSWER 38 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-496929 [54] WPIDS
CROSS REFERENCE: 2001-442253 [47]; 2001-442255 [47]; 2001-451890 [48]; 2001-451908 [48]; 2001-451909 [48]; 2001-451912 [48]; 2001-451938 [48]; 2001-451939 [48]; 2001-457603 [49]; 2001-457740 [49]; 2001-465363 [50]; 2001-465571 [50]; 2001-465578 [50]; 2001-465705 [50]; 2001-476114 [51]; 2001-476164 [51]; 2001-476197 [51]; 2001-476198 [51]; 2001-476199 [51]; 2001-476282 [51]; 2001-476283 [51]; 2001-483140 [52]; 2001-483233 [52]; 2001-488707 [53]; 2001-488788 [53]; 2001-488875 [53]; 2001-488895 [53]; 2001-496930 [54]; 2001-496931 [54]; 2001-496932 [54]; 2001-514838 [56]; 2001-522358 [57]; 2001-565565 [63]; 2001-582152 [65]; 2001-582153 [65]; 2001-589862 [66]; 2001-589934 [66]; 2001-607699 [69]; 2001-611724 [70]; 2001-611725 [70]; 2001-626375 [72]; 2001-626426 [72]; 2001-626432 [72]; 2001-626527 [72]; 2001-639362 [73]; 2002-010428 [01]; 2002-025688 [03]; 2002-062370 [08]; 2002-280918 [32]; 2002-575369 [61]; 2002-590824 [63]; 2002-674924 [72]
DOC. NO. CPI: C2001-149287
TITLE: Novel matrix metalloprotease-like polypeptides useful for treating neurological disease, cancer, heart disease, liver fibrosis, arthritis, gastric ulcer and periodontal disease.
DERWENT CLASS: B04 D16

INVENTOR(S): ASUNDI, V; DRMANAC, R T; GODBOLE, S D; KUO, C; LIU, C; TANG, Y T
PATENT ASSIGNEE(S): (HYSE-N) HYSEQ INC
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001057255	A1	20010809	(200154)*	EN	142

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001031288 A 20010814 (200173)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001057255	A1	WO 2001-US3434	20010202
AU 2001031288	A	AU 2001-31288	20010202

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001031288	A	Based on	WO 200157255

PRIORITY APPLN. INFO: US 2000-713851 20001115; US 2000-496914 20000203; US 2000-560875 20000427

AB WO 200157255 A UPAB: 20021113

NOVELTY - An isolated matrix metalloprotease (MMP)-like polypeptide (I) comprising a sequence having at least 90% identity to a sequence (S1), its translated protein coding portion, mature protein coding portion, extracellular portion or active domain, or a polypeptide with MMP-like activity comprising at least ten consecutive amino acids of S1, is new.

DETAILED DESCRIPTION - S1 comprises a sequence of 459, 17, 442, 30, 34, 49, 21, 44, 14, 13, 11, 16, 20, 12 or 145 amino acids fully defined in the specification.

INDEPENDENT CLAIMS are also included for the following:

(1) an isolated polynucleotide (II) comprising a sequence (S2) of 561, 1709 or 1380 nucleotides fully defined in the specification, its translated protein coding portion, mature protein coding portion, extracellular portion, or active domain;

(2) an isolated polynucleotide encoding a polypeptide with biological activity, which hybridizes to the complement of (II) under stringent hybridization conditions;

(3) an isolated polynucleotide encoding a polypeptide with biological activity, having greater than 90% sequence identity with (II);

(4) an isolated polynucleotide comprising the complement of (II);

(5) a vector (III) comprising (II);

(6) an expression vector (IV) comprising (II);

(7) a host cell (V) genetically engineered to express (II);

(8) a composition (C) comprising (I);

(9) a polynucleotide encoding (I);

(10) an antibody (Ab) specific for (I);

(11) detecting (II) in a sample, by:

(a) contacting the sample with a compound that binds to and forms a complex with (II) for a period sufficient to form the complex and detecting the complex, so that if a complex is detected, (II) is detected; or

(b) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to (II) under such conditions, amplifying a product comprising at least a portion of (II), and detecting the product, thereby detecting (II) in the sample;

(12) detecting (I) in a sample, by contacting the sample with a compound that binds to and forms a complex with (I) under conditions and for a period sufficient to form the complex, and detecting formation of the complex, so that if a complex formation is detected, (I) is detected;

(13) identifying a compound that binds to (I), by:

(a) contacting the compound with (I) under conditions and for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if polypeptide/compound complex is detected, a compound that binds to (I) is identified; and

(b) contacting the compound with (I), in a cell, for a time sufficient to form a polypeptide/compound complex, where the complex drives expression of a reporter gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to (I) is identified;

(14) producing (I);

(15) a kit comprising (I);

(16) a nucleic acid array (VI) comprising (II) or a unique segment of (II) attached to a surface;

(17) treating a subject in need of enhanced activity or expression of (I), by administering (I), (II) or agonist of (I); and

(18) treating a subject in need to inhibit the activity or expression of (I), by administering a polypeptide that competes with (I), a polynucleotide that inhibits the expression of (II), or antagonist of (I).

ACTIVITY - Cytostatic; neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiinflammatory; dermatological; immunosuppressive; antianemic; neuroprotective; nootropic; vulnerary; antiparkinsonian; anticonvulsant; cerebroprotective; antiHIV; virucide; antibacterial; fungicide; immunostimulant; vasotropic; antidiabetic.

MECHANISM OF ACTION - Gene therapy. No supporting data given.

USE - (VI) detects full-matches or mismatches to the polynucleotide or a unique segment of (II) (claimed). (I) and (II) are useful for therapeutic, diagnostic and research purposes. (II) is useful as hybridization probes, oligomers or primers, for polymerase chain reaction (PCR), use in an array, computer-readable media, for chromosome and gene mapping, recombination production of protein, generation of antisense DNA or RNA, and their chemical analogs. (I) is useful for generating antibodies that are useful for detecting or quantitating (I) in tissue, as molecular weight markers and as food supplement.

(I) and (II) are useful for treating and/or preventing neurological disease, cancer, heart disease, liver fibrosis, gastric ulcer, arthritis and periodontal disease, and for wound healing and angiogenesis. (I) and (II) are useful in preventing and/or treating viral infections, melanomas, as immunosuppressant agents for bone marrow and other tissue transplantation patients, immunological disorders such as rheumatoid arthritis, multiple sclerosis, psoriasis, systemic lupus erythematosus and inflammatory bowel disease, and cancer. (I) and (II) are useful for preventing and/or treating disorders mediated by loss or overexpression of MMP-like polypeptide, including psoriasis, multiple sclerosis, periodontitis, and to boost the killer cell and cytolytic activity of leukocytes of human immune deficiency disease patients.

(II) is useful as primer for identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries, as antisense or antigene agents for sequence-specific modulation of gene expression, in the analysis of single base pair mutations in a gene, and as artificial restriction enzymes. (II) is useful to express recombinant protein for analysis, characterization or therapeutic use, as tissue markers, as molecular weight markers on gels, as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions, to

compare with endogeneous DNA sequences in patients to identify potential genetic disorders, as probes to hybridize and thus discover novel, related DNA sequences, as a source of information to derive PCR primers for genetic fingerprinting, as a probe to subtract-out known sequences in the process of discovering other novel polynucleotides, for selecting and making oligomers for attachment to a gene chip or other support, including for examination of expression patterns, to raise anti-protein antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit another immune response.
Dwg.0/2

L144 ANSWER 39 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-336008 [35] WPIDS
DOC. NO. CPI: C2001-103902
TITLE: Detection of compound in cell, useful for e.g. diagnostics and examination of signal transduction pathways, comprises introducing 2 fusion proteins into the cell.
DERWENT CLASS: B04 D16
INVENTOR(S): KOEHLER, F
PATENT ASSIGNEE(S): (KOHL-I) KOHLER F; (KOEH-I) KOEHLER F
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001036671	A2	20010525	(200135)*	EN	82
AU 2001023545	A	20010530	(200152)		

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001036671	A2	WO 2000-EP10943	20001106
AU 2001023545	A	AU 2001-23545	20001106

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001023545	A	Based on	WO 200136671

PRIORITY APPLN. INFO: EP 1999-121887 19991104

AB WO 200136671 A UPAB: 20010625
NOVELTY - Detection of a compound within a cell comprising:
(a) introducing into a cell material containing at least 2 fusion proteins, its derivatives or nucleic acid encoding the fusion proteins;
(b) allowing expression of the nucleic acid, if applicable; and
(c) assessing for a signal from the first or second signaling entity that is provided, restored, altered or influenced, is new.
DETAILED DESCRIPTION - Detection (M1) of a compound within a cell comprising:
(a) introducing into a cell material (I) containing at least 2 fusion proteins (FP), its derivatives or nucleic acid (NA) encoding the fusion proteins, where one of the fusion proteins or its derivatives contains an amino acid (aa) sequence or a non-proteinaceous structure (NPS):
(i) capable of interacting with a first portion of the compound;

(ii) representing or containing a targeting signal for a subcellular structure; and

(iii) representing or containing a first signaling entity; where the second FP contains an aa sequence or a NPS:

(iv) capable of specifically interacting with a second portion of the compound, where the first and second portion are spatially distinct to allow the simultaneous interaction of (i) and (iv) with the compound;

(v) representing or containing a targeting signal specific for the same subcellular structure as (ii); and

(vi) representing or comprising a second signaling entity, where the first and second signaling properties are provided, restored, altered or influenced upon close spatial arrangement of the entities; where the compound or its precursor is present or expressed in the cell before or simultaneously when the material is introduced or expressed;

(b) allowing expression of the NA, if applicable; and

(c) assessing for a signal from the first or second signaling entity that is provided, restored, altered or influenced.

INDEPENDENT CLAIMS are also included for the following:

(1) detection of the fusion of 2 cells or 2 subcellular structures comprising carrying out M1;

(2) detection (M2) of the fusion of 2 cells or 2 subcellular structures;

(3) detection (M3) of ligand-induced receptor internalization;

(4) assessing the suitability of a signal sequence, polypeptide (PP) or a non-proteinaceous compound to direct a further compound into a subcellular structure comprising carrying out M1;

(5) detection (M4) of one or more aa sequences or NPS that interact with spatially distinct but closely arranged portions of a compound;

(6) mapping (M5) groups comprising contacting a compound under investigation for group mapping with 2 different aa sequences or NPS where the first and second aa sequence or NPS are connected with an aa sequence or NPS representing or containing a first and second signaling entity respectively, and the signaling properties of the entities are provided, restored, altered or influenced upon close spatial arrangement of the entities;

(7) kit comprising at least 2 FP, its derivatives or nucleic acid encoding FP for carrying out the above methods;

(8) a cell into which the FP, its derivatives or the nucleic acid encoding FP have been stably introduced;

(9) a cell (II) comprising a compound as described previously and optionally at least one of the FP, its derivatives or the nucleic acid encoding the FP;

(10) a cell stably transfected with nucleic acid encoding at least 2 pairs of FP or its derivatives, where each pair has a targeting signal that is specific for a different cell or subcellular structure as compared to the targeting signal of the other pairs of FP and where each pair of FP generates a signal that is different from any signal generated by the other FP pairs;

(11) assessing the localization of a compound comprising introducing the compound into (II) and assessing the generation of the a signal; and

(12) a vector encoding a nucleic acid as specified previously.

USE - The methods have many uses such as:

(1) examination of signal transduction pathways, where a change in protein localization is involved;

(2) examination of whether substances lead to or inhibit a change in the localization of candidate proteins;

(3) detection of substances binding to surface receptors and subsequent internalization;

(4) examination of inflammatory processes;

(5) diagnosing blood cell diseases or tumors;

(6) examination of chemical industry products for their bioreactivity;

(7) construction of cDNA libraries;

(8) functional screening for ligands of surface receptors; and
(9) assessment of fusion events of cells or subcellular structures.
ADVANTAGE - The method allows the easy introduction of the detection constructs into the living cell which overcomes the time-consuming and laborious steps of prior art. In addition, the cells or their progeny can then be used for further analysis or manipulation.
Dwg.0/9

L144 ANSWER 40 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-235288 [24] WPIDS
DOC. NO. NON-CPI: N2001-168193
DOC. NO. CPI: C2001-070625
TITLE: Assaying libraries of test compounds as ligands and/or substrates of transport proteins, where compounds identified can be linked to pharmaceutical agents therefore facilitating uptake of these agents by a patient.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BARRETT, R W; CHERNOV-ROGAN, T; CUNDY, K C; DOWER, W J; GALLOP, M
PATENT ASSIGNEE(S): (XENO-N) XENOPORT INC
COUNTRY COUNT: 95
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001020331	A1	20010322	(200124)*	EN	139

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2000077034	A	20010417	(200140)		
EP 1212619	A1	20020612	(200239)	EN	

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001020331	A1	WO 2000-US25439	20000914
AU 2000077034	A	AU 2000-77034	20000914
EP 1212619	A1	EP 2000-966735	20000914
		WO 2000-US25439	20000914

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000077034	A	Based on	WO 200120331
EP 1212619	A1	Based on	WO 200120331

PRIORITY APPLN. INFO: US 1999-154071P 19990914
AB WO 200120331 A UPAB: 20010502
NOVELTY - A variety of methods for assaying libraries of test compounds as ligands and/or substrates of transport proteins, including both carrier-type and receptor-type transport proteins, are new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are provided for the following:
(1) a method (M1) of screening for a carrier-type transport protein or a receptor-type transport protein and/or its ligand, comprising:

(a) providing a library comprising different complexes, each complex comprising a compound and a reporter, the compound varying between different complexes;

(b) providing a population of cells, one or more of which expresses one or more carrier-type transport proteins;

(c) contacting the population of cells with a complexes from the library; and

(d) detecting a signal from the reporter of a complex that is bound to a cell or internalized within a cell, the signal providing an indication that a complex whose reporter generated the signal comprises a compound that is a ligand for a carrier-type transport protein;

(2) methods (M2) of screening for a carrier-type transport protein and/or its substrate;

(3) a method (M3) of screening for a substrate of a transport protein, comprising:

(a) introducing into a body compartment of an animal a population of complexes, each complex comprising a support, a test compound, and a reporter, the test compound varying between complexes; and

(b) recovering complexes by means of their reporter from a tissue or fluid of the animal after transport of at least some of the complexes through cells lining the body compartment; and

(4) a pharmaceutical composition comprising a nanoparticle, a drug within or linked to the nanoparticle and a ligand linked to or within the nanoparticle, the ligand being effective to promote cellular uptake and/or transport of the particle by receptor-type transport proteins.

ACTIVITY - None given.

No biological data given.

MECHANISM OF ACTION - None given.

No biological data given.

USE - The methods are used for screening individual or test complexes for activity as ligands for various transport proteins. Compounds identified by the methods can be linked to pharmaceutical agents therefore facilitating uptake of these agents by a patient, for e.g. a substrate for an intestinal epithelial cell transporter can be linked to a pharmaceutical agent via a linker that is either enzymatically and/or chemically cleavable or is non-cleavable.

ADVANTAGE - The methods are amenable to **high throughput** screening formats and can be used to screen large libraries of complexes.

Dwg.0/30

L144 ANSWER 41 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-080984 [09] WPIDS
DOC. NO. NON-CPI: N2001-061668
DOC. NO. CPI: C2001-023387
TITLE: Selection of at least one interacting molecule, useful for **high-throughput** selection of interacting molecules, comprising contacting molecule with second molecule affixed to magnetic particle and washing.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): KONTHUR, Z; LEHRACH, H; WALTER, G
PATENT ASSIGNEE(S): (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
COUNTRY COUNT: 22
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001002554	A2	20010111	(200109)*	EN	27
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
EP 1198566	A2	20020424	(200235)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001002554	A2	WO 2000-EP6271	20000704
EP 1198566	A2	EP 2000-949254	20000704
		WO 2000-EP6271	20000704

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1198566	A2	Based on	WO 200102554

PRIORITY APPLN. INFO: EP 1999-112970 19990705

AB WO 200102554 A UPAB: 20010213

NOVELTY - Selection of at least 1 member of a number of specifically interacting molecules comprising:

(a) contacting a first molecule with a second molecule affixed to a magnetic particle;

(b) subjecting the product to at least 1 washing step;

(c) determining whether a specific interaction between the first and second molecule has occurred; and

(d) providing the first and/or second molecule selected, is new.

DETAILED DESCRIPTION - Selection (M1) of at least 1 member of a number of specifically interacting molecules comprising:

(a) contacting a first molecule with a second molecule affixed to a magnetic particle;

(b) subjecting the product to at least 1 washing step;

(c) determining whether a specific interaction between the first and second molecule had occurred; and

(d) providing the first and/or second molecule selected, where steps (a) to (c) are carried out in container(s), preferably representing an arrayed form, e.g. in (a) microtiter plate(s), using an automated device containing a magnetic particle processor.

An INDEPENDENT CLAIM is also included for the production of a pharmaceutical composition comprising (M1) and formulating the first and/or second molecule selected and/or characterized by (M1) or a functionally and/or structurally equivalent derivative.

USE - The method is used for the **high-throughput** selection of various members of pairs of interacting molecules.

ADVANTAGE - The method allows the number of magnetic particles to be scaled down compared to the manual techniques (e.g. 10-fold to 2 micro l or 1.34x10 to the power of 6 Dynabeads M-280 Streptavidin, Dynal). This causes much less unspecific background binding resulting in a distinct reduction of false positive results. All washing and incubation conditions can be reproducibly customized. Washing speeds are adjusted to cause different stringencies of selection. This enables the predictable selection of interacting molecules with different binding affinities. The method allows **high-throughput** of interacting molecules as large numbers of e.g. library clones can be handled in parallel and the selection of interacting molecules from e.g. 2 libraries can be used to create interaction catalogues.

Dwg.0/6

L144 ANSWER 42 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2000-611723 [58] WPIDS
DOC. NO. CPI: C2000-183125
TITLE: Identifying and characterizing regulon genes, useful e.g. for identifying potential therapeutic target genes for the treatment of diseases associated with a particular MP of interest.

DERWENT CLASS: B04 C06 D16
INVENTOR(S): ASHBY, M; MARINI, N; PHILLIPS, J; SCHERER, S; ZIMAN, M
PATENT ASSIGNEE(S): (ROSE-N) ROSETTA INPHARMATICS INC
COUNTRY COUNT: 92
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000058521	A2	20001005	(200058)*	EN	187

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2000040576 A 20001016 (200106)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000058521	A2	WO 2000-US8604	20000331
AU 2000040576	A	AU 2000-40576	20000331

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000040576	A	Based on	WO 200058521

PRIORITY APPLN. INFO: US 1999-127223P 19990331

AB WO 200058521 A UPAB: 20001114
NOVELTY - Methods for identifying and characterizing genes whose expression is indicative of activation of a metabolic pathway (MP) or common set of biochemical reactions in a cell (i.e. regulon indicator genes) and for characterizing a gene (GnX) of unknown function by determining which MP or common set of biochemical reactions it is associated with to place the gene in a genetic group (regulon).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

(1) placing (I) GnX into a functional genetic group, comprising:

(a) generating a gene expression profile (GEP) for GnX;

(b) comparing the GEP of GnX with GEPs of a number of other genes in a data base of compiled GEPs to generate expression correlation coefficiencies (CCs);

(c) identifying (based on their expression CCs) a set of genes comprising GnX that are coordinately expressed;

(d) determining if the gene(s) whose expression is most highly correlated with that of GnX belong to a gene regulon involved in a known biological pathway, or a common set of biological reactions or functions; and

(e) optionally testing the effects on GnX expression of at least 1 altered condition or treatment known to affect the function to which GnX has been ascribed (GnX is placed in the regulon region of d) if GnX expression is coordinate with expression of that regulon;

(2) identifying (II) a regulon indicator gene in a data base of compiled GEPs, in which expression of the regulon indicator gene correlates with the expression of at least 1 known gene in a group of coordinately expressed genes or provide a measure of the function of a biological process of interest, comprising:

(a) comparing GEPs of a number of genes in the database to generate expression CCs;

(b) identifying (based on their relative expression CCs) a set of

genes that are coordinately expressed ;

(c) selecting a set of genes from b) which comprises 1 or more genes known to function in a particular biological pathway, or a common set of biological reactions of functions;

(d) selecting a member of the set of c) having 1 or more of the following characteristics:

(i) its expression profile (EP) is sensitive to one or more stimuli;

(ii) its EP exhibits a large dynamic range in response 1 or more stimuli;

(iii) its EP exhibits a rapid kinetic response to 1 or more stimuli;

(iv) it EP is specific to a known biological pathway or a common set of biological reactions or functions; and

(v) the regulon indicator gene does not contain sequences that are problematic for maintaining on plasmids when introduced into host cells;

(3) selecting (III) a novel regulon target gene from a database of compiled GEPs, comprising:

(a) comparing GEPs for a number of genes in the database to generate expression CCs;

(b) identifying based on the CCs, a set of genes that are coordinately expressed;

(c) selecting from b) a set of genes comprising one or more genes of unknown function and 1 or more genes known to function in a particular biological pathway or common set of biological reactions or functions of interest; and

(d) selecting from c) at least 1 gene of unknown function, GnX, as a novel regulon target gene (GnX is a gene whose EP closely correlates to the EPs of 1 or more of the genes of the set of c) known to function in the particular biological pathway or common set of biological reaction or function of interest;

(4) identifying (IV) a potential inhibitor of a regulon target gene, comprising:

(a) incubating a polypeptide comprising an amino acid sequence encoded by a regulon target gene with a candidate compound under conditions that promote specific binding between the polypeptide and the compound; and

(b) determining whether the polypeptide bound to the compound (the compound is a potential inhibitor if the compound binds to the polypeptide;

(5) identifying (V) a potential inhibitor of a regulon target gene;

(6) inhibiting (VI) the expression of a regulon target gene in a host cell, comprising introducing an inhibitor (produced by the methods above) into the host cell;

(7) antisense oligonucleotides (VII) comprising a sequence complementary to the sequence of an mRNA of a regulon target gene which decreases transcription or translation of the gene;

(8) ribozymes (VIII) comprising a sequence complementary to the sequence of an mRNA of a regulon target gene which decreases transcription or translation of the gene;

(9) neutralizing antibodies (IX) to a protein encoded by a regulon target gene of a yeast or its mammalian homolog;

(10) fusion proteins (X) comprising an amino acid sequence encoded by a regulon target gene of a yeast or its mammalian homolog and further comprising a group tag or reporter gene;

(11) identifying (XI) a gene regulated by a regulon target gene of a yeast or its mammalian homolog; and

(12) identifying (XII) a regulon indicator gene in a database of compiled GEPs (expression of the regulon indicator gene provides a measure of the function of a biological pathway or process of interest);

USE - The methods are used for identifying and characterizing genes whose expression is indicative of activation of a MP or common set of biological/biochemical reactions in a cell (i.e. regulon indicator genes) and for characterizing a gene (GnX) of unknown function by determining which MP or common set of biological/biochemical reactions it is

associated with to place the gene in a genetic group or regulon. The methods may also be used to identify desirable therapeutic targets in biological pathways of interest (i.e. regulon target genes).
Dwg.0/75

L144 ANSWER 43 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2000-594641 [56] WPIDS
DOC. NO. NON-CPI: N2000-440347
DOC. NO. CPI: C2000-177658
TITLE: Identifying a target gene for design or discovery of an antifungal agent, insecticide, or herbicide, comprising disrupting the function of a gene in a yeast cell and identifying whether the function is essential for e.g. germination.
DERWENT CLASS: B04 C07 D16 S03
INVENTOR(S): DIMSTER-DENK, D; DIMSTER-DENK, D F
PATENT ASSIGNEE(S): (ROSE-N) ROSETTA INPHARMATICS INC
COUNTRY COUNT: 92
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000058457	A2	20001005	(200056)*	EN	154
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000041866	A	20001016	(200106)		
US 2002103154	A1	20020801	(200253)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000058457	A2	WO 2000-US8641	20000331
AU 2000041866	A	AU 2000-41866	20000331
US 2002103154	A1 Provisional	US 1999-127272P	19990331
	Div ex	US 2000-539697	20000331
		US 2001-965602	20010927

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000041866	A Based on	WO 200058457

PRIORITY APPLN. INFO: US 1999-127272P 19990331; US 2000-539697 20000331; US 2001-965602 20010927

AB WO 200058457 A UPAB: 20001106
NOVELTY - A method (M1) for identifying a target gene for design or discovery of an antifungal agent comprising disrupting the function of a gene in a yeast cell, and identifying whether the function is essential for germination, growth, pseudohyphal growth or hyphal growth, is new.

DETAILED DESCRIPTION - A method (M1) for identifying a target gene for design or discovery of an antifungal agent comprising disrupting the function of a gene in a yeast cell, and identifying whether the function is essential for germination, growth, pseudohyphal growth or hyphal growth, is new.

The method further comprises determining whether the protein encoded by the essential gene has homology to a human, non-human mammal, insect or plant protein.

INDEPENDENT CLAIMS are also included for the following:
(1) a method (M2) for identifying a target for design or discovery of a herbicide, insecticide, or antiproliferation agent comprising:
(a) disrupting the function of a gene in a yeast cell;
(b) identifying whether the function of the gene is essential for yeast germination, vegetative growth, pseudohyphal or hyphal growth;
(c) selecting the gene if it is essential; and
(d) determining whether the protein encoded by the essential gene has homology to a plant, insect, or non-human mammalian protein for design of a herbicide, insecticide, or antiproliferation agent, respectively;
(2) an antisense oligonucleotide or ribozyme comprising a sequence complementary to the sequence of an mRNA of an essential gene, which decreases transcription or translation of the essential gene;
(3) a neutralizing antibody to a protein encoded by an essential gene of a yeast;
(4) a fusion protein comprising an amino acid sequence encoded by an essential gene of a yeast and further comprising an epitope tag or reporter gene;
(5) a method (M3) for identifying genes regulated by the essential gene comprising:
(a) overexpressing the essential gene in cells of a Genome Reporter Matrix; and
(b) identifying genes that are either induced or repressed by overexpression of the essential gene;
(6) a method (M4) for identifying potential antifungal compounds comprising:
(a) as (a) in M3;
(b) as (b) in M3; and
(c) screening compounds on the subset of genes, where a compound is a potential antifungal compound of it downregulates a gene that is induced by overexpression of the essential gene or if it upregulates a gene that is repressed by overexpression of the essential gene; and
(7) a method (M5) to identify a potential antifungal compound comprising:
(a) incubating a polypeptide comprising an amino acid sequence encoded by an essential gene with a compound under conditions to promote specific binding between the polypeptide and the compound; and
(b) determining whether the polypeptide bound to the compound.
USE - The methods are useful for identifying genes in Saccharomyces cerevisiae which are essential for germination and proliferation of S. cerevisiae and using the identified genes or their encoded proteins as targets for highly specific antifungal agents, insecticides, herbicides and antiproliferation drugs.
Dwg.0/37

L144 ANSWER 44 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2000-038358 [03] WPIDS
CROSS REFERENCE: 1995-382985 [49]; 1998-286866 [25]; 1999-229499 [19]; 1999-229532 [19]; 1999-229533 [19]; 1999-254381 [21]; 1999-254713 [21]; 1999-302739 [25]; 1999-326705 [27]; 1999-337420 [28]; 1999-347718 [29]; 1999-371118 [31]; 1999-404743 [34]; 1999-430385 [36]; 1999-551358 [46]; 1999-580306 [49]; 1999-620728 [53]; 2000-062031 [05]; 2000-072883 [06]; 2000-116314 [10]; 2000-237871 [20]; 2000-271386 [23]; 2000-271431 [23]; 2000-271434 [23]; 2000-271435 [23]; 2000-292842 [25]; 2000-317943 [27]; 2000-412154 [35]; 2000-412324 [35]; 2000-412325 [35]; 2000-431586 [37]; 2000-442668 [38]; 2000-452188 [39]; 2000-452395 [39]; 2000-499263 [44]; 2000-572269 [53]; 2000-572270 [53]; 2000-572271 [53]; 2000-587437 [55]; 2000-594320 [56]; 2000-594321 [56]; 2000-611443 [58]; 2000-611444 [58]; 2000-628263 [60]; 2000-638138 [61]; 2000-638201 [61]; 2000-679484 [66]; 2001-016509 [02];

2001-025022 [03]; 2001-025251 [03]; 2001-025253 [03];
2001-032160 [04]; 2001-050025 [06]; 2001-050091 [06];
2001-070561 [08]; 2001-071075 [08]; 2001-071078 [08];
2001-071395 [08]; 2001-081051 [09]; 2001-090793 [10];
2001-091968 [10]; 2001-103149 [11]; 2001-183260 [18];
2001-226690 [23]; 2001-226823 [23]; 2001-235264 [24];
2001-381383 [40]; 2001-381384 [40]; 2001-408281 [43];
2001-451708 [48]; 2001-541567 [60]; 2001-541628 [60];
2001-602746 [68]; 2001-625876 [72]; 2002-075461 [10];
2002-090516 [12]; 2002-130120 [17]; 2002-130151 [17];
2002-130882 [17]; 2002-171999 [22]; 2002-172001 [22];
2002-205567 [26]; 2002-256031 [30]; 2002-280917 [32];
2002-280928 [32]; 2002-280940 [32]; 2002-292065 [33];
2002-362426 [39]; 2002-383270 [41]; 2002-404358 [43];
2002-487624 [52]; 2002-657277 [70]; 2002-665999 [71];
2002-673823 [72]; 2002-690475 [74]; 2002-713224 [77]

DOC. NO. NON-CPI: N2000-028952
DOC. NO. CPI: C2000-009747
TITLE: New isolated GFR-alpha3 **nucleic acid**, used to develop products for treating diseases or conditions involving peripheral nervous system or automic nervous system.
DERWENT CLASS: B04 C03 C06 D16 S03
INVENTOR(S): DE SAUVAGE, F J; KLEIN, R D; PHILLIPS, H S; ROSENTHAL, A; ASHKENAZI, A; GODDARD, A; GURNEY, A L; NAPIER, M; WOOD, W I; YUAN, J
PATENT ASSIGNEE(S): (GETH) GENENTECH INC
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9949039	A2	19990930	(200003)*	EN	112
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZA ZW					
AU 9931944	A	19991018	(200009)		
EP 1064376	A2	20010103	(200102)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
US 2002010137	A1	20020124	(200210)		
JP 2002507421	W	20020312	(200220)		181
MX 2000009215	A1	20010501	(200227)		
ZA 2000004686	A	20020626	(200251)		137
NZ 506748	A	20021025	(200274)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9949039	A2		WO 1999-US6098	19990319
AU 9931944	A		AU 1999-31944	19990319
EP 1064376	A2		EP 1999-913993	19990319
			WO 1999-US6098	19990319
US 2002010137	A1	Provisional	US 1997-59263P	19970918
		Provisional	US 1997-59836P	19970924
		Provisional	US 1997-63561P	19971028
		Provisional	US 1997-64248P	19971103
		Provisional	US 1998-79124P	19980323
		Provisional	US 1998-81569P	19980413
		Provisional	US 1998-99803P	19980910

	Provisional	US 1998-104080P	19981013
	Provisional	US 1999-123957P	19990312
	Provisional	US 1999-131445P	19990428
	Provisional	US 1999-144758P	19990720
	Provisional	US 1999-145698P	19990726
	Cont of	US 2000-565278	20000427
		US 2001-828366	20010405
JP 2002507421 W		WO 1999-US6098	19990319
		JP 2000-538000	19990319
MX 2000009215 A1		MX 2000-9215	20000920
ZA 2000004686 A		ZA 2000-4686	20000906
NZ 506748 A		NZ 1999-506748	19990319
		WO 1999-US6098	19990319

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9931944	A	Based on	WO 9949039
EP 1064376	A2	Based on	WO 9949039
JP 2002507421 W		Based on	WO 9949039
NZ 506748	A	Based on	WO 9949039

PRIORITY APPLN. INFO: US 1998-81569P 19980413; US 1998-79124P 19980323; WO 1998-US17888 19980828; WO 1998-US18824 19980910; WO 1998-US19330 19980916; WO 1999-US20594 19990908; WO 1999-US21090 19990915; WO 1999-US23089 19991005; WO 1999-US28313 19991130; WO 1999-US28564 19991202; WO 1999-US30999 19991220; WO 2000-US219 20000105; WO 2000-US277 20000106; WO 2000-US4414 20000222; WO 2000-US5841 20000302; WO 2000-US6319 20000310; WO 2000-US6884 20000315; WO 2000-US32678 20001201

AB WO 9949039 A UPAB: 20021204

NOVELTY - Isolated glial-cell-line-derived neurotrophic factor family receptor alpha -3 (GFR alpha 3) polypeptides and **polynucleotides** are new.

DETAILED DESCRIPTION - A novel isolated (A) **nucleic acid** (NA) comprises a NA having at least a 65 % sequence identity to:

(a) NA molecule (NAM) encoding a GFR alpha 3 polypeptide comprising the sequence of amino acids 27 to 400 of sequence (XV) shown (400 amino acids in length) or the sequence of amino acids 27 to 369 of sequence (XVII) (369 amino acids in length); or

(b) the complement of an NAM as in (a).

INDEPENDENT CLAIMS are also included for the following:

(1) an isolated NA comprising NA having at least a 65% sequence identity to:

(a) NAM encoding the same mature polypeptide encoded by a cDNA in ATCC No. 209752 (DNA48613-1268) or in ATCC No. 209751; or

(b) the complement of a DNA molecule as in (a);

(2) an isolated NA comprising an NA having at least a 65% sequence identity to:

(a) NAM encoding a GFR alpha 3 polypeptide comprising a sequence of amino acids 84 to 360 of sequence (XV), amino acids 84 to 329 of sequence (XVII), or a sequence of amino acids 110 to 386 of sequence (XX) (888 amino acids in length); or

(b) the complement of an NAM as in (a);

(3) a vector comprising an NA as in (A);

(4) a host cell comprising a vector as in (3);

(5) a polypeptide comprising a sequence having at least 65% sequence

identity with amino acid residues 84 to 360 of sequence (XV) or 84 to 329 of sequence (XVII);

(6) a chimeric molecule comprising a GFR alpha 3 polypeptide fused to a heterologous amino acid sequence;

(7) an **antibody** which specifically binds to GFR alpha 3 polypeptide;

(8) measuring agonist binding to a polypeptide comprising an agonist-binding domain of an alpha -subunit receptor, comprising exposing the polypeptide positioned in a cell membrane to a candidate agonist and measuring homo-dimerization or homo-oligomerization of the polypeptide;

(9) measuring autophosphorylation of a polypeptide receptor construct comprising a ligand-binding domain of an alpha -subunit receptor, the intracellular catalytic domain of a tyrosine kinase receptor (TKR), and a flag epitope comprising:

(a) coating a first solid phase with a homogeneous population of eukaryotic cells so that the cells adhere to the first solid phase, where, positioned in their membranes, the cells have the polypeptide receptor construct;

(b) exposing the adhering cells to an analyte;

(c) solubilizing the adhering cells, thereby releasing cell lysate;

(d) coating a second solid phase with a **capture agent** which binds specifically to the flag epitope so that the **capture agent** adheres to the second solid phase;

(e) exposing the adhering **capture agent** to the cell lysate obtained in (c) so that the receptor construct adheres to the second solid phase;

(f) washing the second solid phase so as to remove unbound cell lysate;

(g) exposing the adhering receptor construct to an anti-phosphotyrosine **antibody** which identifies phosphorylated tyrosine residues in the TKR; and

(h) measuring binding of the anti-phosphotyrosine **antibody** to the adhering receptor construct;

(10) measuring autophosphorylation of a polypeptide receptor construct comprising a ligand-binding domain of an alpha -subunit receptor, the intracellular catalytic domain of a TKR, and a flag epitope;

(11) a polypeptide comprising an alpha -subunit receptor ligand-binding domain, a flag polypeptide, and an intracellular catalytic domain of a TKR;

(12) a kit comprising a solid phase coated with a **capture agent** which binds specifically to a flag polypeptide, and a polypeptide comprising an alpha -subunit receptor ligand-binding domain, a flag polypeptide, and an intracellular catalytic domain of a TKR; and

(13) an assay for measuring phosphorylation of polypeptide receptor construct comprising a ligand-binding domain of an alpha -subunit receptor, the intracellular catalytic domain of a kinase receptor, and a flag epitope.

USE - The GFR alpha 3 polypeptides possess neuronal cell activation function typical of the GFR protein family. GFR alpha 3 ligands can be used to stimulate proliferation, growth, survival, differentiation, metabolism or regeneration of GFR alpha 3- and Ret-containing cells. Agents which bind to the GFR alpha 3 molecule could be useful in the treatment of diseases or conditions involving the peripheral nervous system, e.g. such ligands can be used to treat peripheral neuropathies associated with diabetes, human immunodeficiency virus (HIV), or chemotherapeutic agent treatments. Ligands binding to GFR alpha 3 are expected to be useful in the treatment of neuropathic pain, antagonists of GFR alpha 3 are expected to be useful to treat chronic pain of non-neuropathic nature e.g. that which is associated with various inflammatory states. GFR alpha 3 or its agonist or antagonists can be used to treat conditions involving dysfunction of the autonomic nervous system including disturbances in blood pressure or cardiac rhythm, gastrointestinal function, impotence, and urinary continence. Other

indications for ligands binding to GFR alpha 3 include post-herpetic neuralgia, shingles, asthma, irritable bowel, inflammatory bowel, cystitis, headache (migraine), arthritis, spinal cord injury, constipation, hypertension, mucositis, dry mouth or eyes, fibromyalgia, chronic back pain, or wound healing. Ligands which act via GFR alpha 3 will be particularly useful to treat disorders of the peripheral nervous system while inducing fewer effects on weight loss, motor function, or on kidney function than would ligands acting via GFR alpha 1 or GFR alpha 2. The products and methods can also be used for qualitatively and quantitatively measuring alpha -subunit receptor activation as well as facilitating identification and characterization of potential agonists and antagonists for a selected alpha -subunit receptor. The products can also be used for detection, diagnosis and production of transgenic animals. Dwg.0/13

L144 ANSWER 45 OF 45 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1999-263481 [22] WPIDS
CROSS REFERENCE: 1997-179271 [16]
DOC. NO. CPI: C1999-077680
TITLE: **Nucleic acid** encoding telomere repeat binding factor for treatment of, e.g. cancer.
DERWENT CLASS: B04 D16
INVENTOR(S): BROCCOLI, D; DE LANGE, T; SMOGORZENSKA, A; LANGE, T D; DELANGE, T
PATENT ASSIGNEE(S): (UYRQ) UNIV ROCKEFELLER; (BROC-I) BROCCOLI D; (LANG-I) LANGE T D; (SMOG-I) SMOGORZENSKA A
COUNTRY COUNT: 83
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9915662	A1	19990401	(199922)*	EN	160
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW					
AU 9897774	A	19990412	(199934)		
EP 1017812	A1	20000712	(200036)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
US 6297356	B1	20011002	(200160)		
US 2002076719	A1	20020620	(200244)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9915662	A1		WO 1998-US20175	19980925
AU 9897774	A		AU 1998-97774	19980925
EP 1017812	A1		EP 1998-951953	19980925
			WO 1998-US20175	19980925
US 6297356	B1	CIP of	US 1995-519103	19950825
		CIP of	US 1997-938052	19970926
			US 1998-18635	19980204
US 2002076719	A1	CIP of	US 1995-519103	19950825
		CIP of	US 1997-938052	19970926
		Div ex	US 1998-18635	19980204
			US 2001-912962	20010725

FILING DETAILS:

PATENT NO	KIND	PATENT NO

AU 9897774	A	Based on	WO 9915662
EP 1017812	A1	Based on	WO 9915662
US 6297356	B1	CIP of	US 5733730
US 2002076719	A1	CIP of	US 5733730
		Div ex	US 6297356

PRIORITY APPLN. INFO: US 1998-18635 19980204; US 1997-938052 19970926; US 1995-519103 19950825; US 2001-912962 20010725

AB WO 9915662 A UPAB: 20020711

NOVELTY - Isolated **nucleic acid** (I) encoding a vertebrate telomere repeat binding factor (TRF), designated TRF2, that is homologous with a human 500 amino acid sequence (S1) (given in the specification), and contains:

(i) a basic N-terminal domain (NTD);

(ii) a dimerization domain (DD), and

(iii) a Myb domain (MD). When NTD is removed, TRF binds detectably to the telomere repeat sequence (TTAGGG)12.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) unicellular hosts transformed or transfected with (I) that is linked to an expression control sequence;

(2) pure TRF produced by these hosts;

(3) isolated **nucleic acids** (Ia) encoding one of NTD, DD or a truncated TRF;

(4) TRF encoded by (I);

(5) proteolytic fragments of TRF;

(6) isolated NTD, DD or truncated TRF;

(7) **antibodies** that recognize NTD; and

(8) immmortalized cell lines that produce monoclonal **antibodies** of (7).

ACTIVITY - Anticancer; anti-aging.

MECHANISM OF ACTION - TRF maintains the correct structure of telomere termini and protects against end-to-end fusion. It is required for cell proliferation. When HTC75 cells were transformed with vector pUHD10-3 modified with the full-length sequence for TRF2, no significant effect on short-term cell growth was observed. Overexpression of TRF2 in which the Myb domain had been deleted caused almost complete inhibition of growth after 4 days. The treated cells shows characteristic signs of senescence, with anaphase bridges and lagging chromosomes, indicating induction of chromosome end fusions.

USE - Cells transformed with (I) are used to produce TRF or its individual domains. TRFs (or their antagonists and agonists) can be used to limit reduction in telomere length associated with aging (e.g. atrophy of the skin, age-related macular degeneration and atherosclerosis) or abnormal telomere lengths in cancer cells. They can also be used to screen for specific modulators (potentially useful for treating aging and cancer), including those that are specific for one TRF over another; to diagnose telomere-associated disorders; as targeting agents for TTAGGG repeats and in construction of mammalian artificial chromosomes (for gene therapy or basic research). **Antibodies** against TRF can be used for diagnosis and therapy, e.g. to differentiate between different TRFs to screen expression **libraries** for TRF-expressing genes or to detect (pre)cancers or viral infections. (I), or their fragments, are used as probes to screen genomic and cDNA **libraries**, and for expression of antisense RNA or ribozymes.

ADVANTAGE - None given.

Dwg.0/19

FILE 'HOME' ENTERED AT 11:48:02 ON 09 DEC 2002